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(54) **WNT COMPOSITIONS AND THERAPEUTIC USES OF SUCH COMPOSITIONS**

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See application file for complete search history.

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(57) **ABSTRACT**

The invention provides novel Wnt polypeptides that have enhanced solubility and improved biologic drug-like properties, and polynucleotides encoding the Wnt polypeptides of the invention. The Wnt polypeptides of the invention can be used therapeutically, such as, for example, in methods of preventing or treating muscle loss and/or promoting muscle hypertrophy and growth.

18 Claims, 16 Drawing Sheets

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Wnt-1	-----MGLWALLPGW-----VSATLLLLALAALPAALA	27
Wnt-2	-----MNAPLG-----GIWLWLPLLLTWLTP	21
Wnt-2b	-----MLDGLGVV-----AISIFGIQLKTEGSLRTAVP	28
Wnt-3	-----MEPH-----LLGLLLGLLLGGTRVLA	21
Wnt-3a	-----MAP-----LGYFL-LLCSLKQALG	18
Wnt-4	-----MSPR-----SCLRSRLLVFAVESAA	21
Wnt-5a	-----MKKSIGILSPGVALGMAGSAMSSKFFLVALAIFFSFAQVVI	41
Wnt-5b	-----MPSLLLLLFTAAALLSSWAQLLT	21
Wnt-6	-----MLPPLPSRLGLLLLLL	16
Wnt-7a	-----MNRKARRC-----LGHLFSLG--MVYLRI	23
Wnt-7b	-----MHRNFRKW-----IFYVFLCFG--VLYVKL	23
Wnt-8a	-----MGNLFMLWAALGIC---C	15
Wnt-8	-----MFLSKPSVYICLFTC	15
Wnt-9a	-----MLDGSPLARWLAAAFGLTLLA	22
Wnt-9b	-----MR--PPPALALAGLC---LLA	16
Wnt-10a	MGSAHPRP-----WLRLRPQPQPPALWVLLFFLL	30
Wnt-10b	-----MLEEPRPRPPPSGLAGLLFLA	21
Wnt-11	-----MRARPQVCEALLFAL	15
Wnt-16	-----MDRAALLG-----LARLCAALWAALLVLFY	25
Wnt-1	ANSSGRWWGIVNVASSTNLLTD-----SKSLQLVLEPSLQLLSRKQRR	70
Wnt-2	EVNSSWWY-----MRATGGS-----SRVMCDNVPGLVSSQRQ	53
Wnt-2b	GIPTQSAFNKC---LQRYIGAL-----G---ARVICDNIPGLVSRQQR	65
Wnt-3	GYP--IWWSLALGQOYTSLGS-----QPLLCGSIPGLVPRQLR	57
Wnt-3a	SYP--IWWSLAVGPQYSSLSGS-----QPILCASIPGLVPRQLR	54
Wnt-4	ASN---WLYLAKLSSVGSISE-----EETCEKLGKLIQRQVQ	55
Wnt-5a	EANSWWSLGMNPNVQMSEVYII-----G---AQPLCSQLAGLSQCQQR	81
Wnt-5b	DANSWWSLALN-PVQRPMEFII-----G---AQPVCSQLPGLSPGQRK	60
Wnt-6	LCPAHVGG-----LWWAVGSP-----LVMDPTSICRKARRLAGRQAE	53
Wnt-7a	GGFSSVVA-----LGAS-----IICNKIPGLAPRQRA	50
Wnt-7b	GALSSVVA-----LGAN-----IICNKIPGLAPRQRA	50
Wnt-8a	AAFSASAWS-----VNNFLIT	31
Wnt-8	VLQLSHSWS-----VNNFLMT	31
Wnt-9a	ALRPSAAYFGLTGSEPLTILP--LTLEPEAAAQAHYKACDRKLKLERKQRR	70
Wnt-9b	LPAAAASYFGLTGREVLTPFPGLGTAAAPAQGGAHKQCDLLKLSRRQKQ	66
Wnt-10a	LLAAAMPERSAPNDIIDLRLPPE-----PVLNANTVCLTLPGLSRRQME	73
Wnt-10b	LCSRALS---NEILGLKLPGE-----PPLTANTVCLTSLGSLSKRQLG	60
Wnt-11	ALQTYGVCYGIKWLALSKTPSAL-----ALN-QTQHCQLEGLVSAQVQ	57
Wnt-16	GAQGNWMW-----LGIASFGV-----P---EKLGCANLP-INSRQKE	58
Wnt-1	LIRQNPGLILHSVSGGLQSAVRECKWQFRNRWNC-----TAPG-PHL	112
Wnt-2	LCHRPDVMRAISQGVAEWTAECQHQFRHRWNCN-----TLDRDHS	96
Wnt-2b	LCQRYPDIMRSVGEAREWIRECQHQFRHRWNC-----TLDRDHTV	108
Wnt-3	FCRNYEIMPSVAEGVKLGIECQHQFRGRWNC-----TIDDSLAI	100
Wnt-3a	FCRNYVEIMPSVAEGIKIGIECQHQFRGRWNC-----TVHDSLAI	97
Wnt-4	MCKRNLEVMDSVRRGAQLAIECQYQFRNRWNC-----TLDS-LPV	97
Wnt-5a	LCHLYQDHMQYIGEGAKTGIKECQYQFRHRWNC-----TVD-NTSV	123
Wnt-5b	LCQLYQEHMAYIGEGAKTGIKECQHQFRGRWNC-----TAD-NASV	102
Wnt-6	LCQAEPEVVAELARGARLGVRECQYQFRFRWNC-----SHS-----KA	93

FIG. 1

Wnt-7a	ICQSRPDAlIIVIGEGSQMGLDECQFQFRNGRWNCs-----ALGERTV	92
Wnt-7b	ICQSRPDAlIIVIGEGAQMGINECQYQFRFGRWNCs-----ALGEKTV	92
Wnt-8a	GPKAYLIYSSSSVAAGAQSGIEECKFQFAWERWNCp-----ENALQLS	73
Wnt-8	GPKAYLIYSSSSVAAGAQSGIEECKYQFAWDRWNCp-----ERALQLS	73
Wnt-9a	MCRRDpGVAETLVEAVSMSALECQFQFRFERWNCt-----LEGry	110
Wnt-9b	LCRRpGLAETLRDAAHLGLLECQFQFRHERWNCs-----LEG--	104
Wnt-10a	VCVRHPDVAASAIQGIQIAIHECQHQRDQRWNCs-----SLETRNKIPY	118
Wnt-10b	LCLRNPdVTASALQGLHIAVHECQHQLRDQRWNCs-----ALEGGGRLPH	105
Wnt-11	LCRSNLELMHTVVHAAREVMKACRRAFADMRWNCs-----SIELAPN	99
Wnt-16	LCKRKPYLLPSIREGARLGIECGSQFRHERWNCMITAAATTAPMGASPL	108
Wnt-1	FGKIVNRGCRETAFIFAITSAGVTHSVARSCSEGSIESCTCDYRRRGPG-	161
Wnt-2	FGRVLLRSSRESAFVYAISSAGVVFAITRACsQGEVKSCSDPKKMGSak	146
Wnt-2b	FGRVMLRSSREAFAFYAISSAGVVHAITRACsQGEVSCSDPYTRGRHH	158
Wnt-3	FGPVLDKATRESAFVHAIASAGVAFVTRSCAEGTSTICGCDShHKGPp-	149
Wnt-3a	FGPVLDKATRESAFVHAIASAGVAFVTRSCAEGTAAICGCSsRHQGS-	146
Wnt-4	FGKVVTQGTREAAFYAISSAGVAFVTRACSSGELEKCGCDRTVHGVS-	146
Wnt-5a	FGRVMQIGSRETAFTHAVSAAGVVNAMSRAcREGELSTCGCS--RAARPK	171
Wnt-5b	FGRVMQIGSRETAFTHAVSAAGVVNAISRACREGELSTCGCS--RTARPK	150
Wnt-6	FGRIQQDIRETAFVFAITAAGASHAVTQACSMGELLQCGCQAPRG----	139
Wnt-7a	FGKELKVGsREAFTYAIIAAGVAHAITAACTQGNLSDCGCDKEKQGQYH	142
Wnt-7b	FGQELRVGSREAFTYAITAAGVAHAVTAACsQGNLSNCGCDREKQGYYN	142
Wnt-8a	THNRLRSATRETSFIHAISSAGVMYITKNCSMGDFENCgCDGSNNGKTG	123
Wnt-8	SHGGRLRSANRETAfVHAISSAGVMYTLTRNCsLGDfDNCgCDDSRNGQLG	123
Wnt-9a	RASLLKRGfKETAFLYAISSAGLTHALAKACSAGRMERCTCDEAPDLENR	160
Wnt-9b	RMGLLKRGfKETAFLYAVSSAALTHTLARACSAGRMERCTCDDSPGLESR	154
Wnt-10a	ESPIFSRGfRESAFAYIAAAGVVHAVSNACALGKLKACGCDASRRGDEE	168
Wnt-10b	HSAILKRGfRESAFSfSMLAAGVMHAVATACSLGKLVS CGCGWKGSGEQD	155
Wnt-11	YLLDLERGtRESAFVYALSAAAIshAIARACTSGDLPGCSCGPVPGEPP-	148
Wnt-16	FGYELSSGTKETAFIYAVMAAGLVHsVTRSCSAGNMTECSCDttLQNGGS	158
Wnt-1	-----GPDWHWGGCSDNI	174
Wnt-2	D-----SKGLFDWGGCSDNI	161
Wnt-2b	D-----QRGDFDWGGCSDNI	173
Wnt-3	-----GEGWKWGGCSEDA	162
Wnt-3a	-----GKGWKWGGCSEDI	159
Wnt-4	-----PQGFQWSGCSDNI	159
Wnt-5a	D-----LPRDWLWGGCGDNI	186
Wnt-5b	D-----LPRDWLWGGCGDNI	165
Wnt-6	-----RAPPRPSGLP-GTPGP-PGPAGSPEGsAAWEGGCGDDV	176
Wnt-7a	R-----DEG-WKWGGCSADI	156
Wnt-7b	Q-----AEG-WKWGGCSADV	156
Wnt-8a	-----GHGWIWGGCSDNV	136
Wnt-8	-----GQGWLWGGCSDNV	136
Wnt-9a	E-----AWQWGGCGDNL	172
Wnt-9b	Q-----AWQWGVCGDNL	166
Wnt-10a	AFRRKLHRLQLDALQRGKGLSHGVPEHPALPTASpGLQDSWEWGGCSPDM	218
Wnt-10b	RLRAKL---LQLQALSRGKSfPHSLPSPGPGSSPSPGPQDTWEWGGCNHDM	203
Wnt-11	-----GPGNRWGGCADNL	161
Wnt-16	A-----SEG-WHWGGCSDDV	172
Wnt-1	DFGRlFGREfVDSGEKGR-----DLRFLMNLHNNEAGRTTVfSEMRQ	216

FIG. 1 (Continued)

Wnt-2 DYGIKFARAFVDAKERKKG-----KDARALMNLHNNRAGRKAVKRFLKQ 204
Wnt-2b HYGVRFAKAFVDAKEKRL-----KDARALMNLHNNRCGRTAVRRFLKL 216
Wnt-3 DFGVLVSREFADARENRP-----DARSAMNKHNNNEAGRRTTILDHMH 204
Wnt-3a EFGGMVSREFADARENRP-----DARSAMNRHNNNEAGRQAIASHMH 201
Wnt-4 AYGVAFSQSFVDVRERSKG-----ASSSRALMNLHNNNEAGRKAILTHMRV 204
Wnt-5a DYGYRFAKEFVDARERERIHA KGSYESARILMNLHNNNEAGRRTVYNLADV 236
Wnt-5b EYGYRFAKEFVDAREREKNFAKGSEEQGRVLMNLQNNNEAGRRAVYKMADV 215
Wnt-6 DFGDEKSRLEFMDARHKRG-----RGDIRALVQLENNNEAGRLAVRSHTRT 220
Wnt-7a RYGIGFAKVFVDAREIKQN---ART-----LMNLHNNNEAGRKILEENMKL 198
Wnt-7b RYGIDFSRRFVDAREIKKN---ARR-----LMNLHNNNEAGRKVLEDRMQL 198
Wnt-8a EFGERISKLFVDSLEKGKD-----ARALMNLHNNRAGRRLAVRATMKR 178
Wnt-8 GFGEAISQVFVDALETGQD-----ARAAMNLHNNNEAGRKAVKGTMKR 178
Wnt-9a KYSSKFVKEFLG-RRSSKD-----LRARVDFHNNLVGVKVIKAGVET 213
Wnt-9b KYSTKFLSNFLGSKRGNKD-----LRARADAHNTHVGIAVKVSGLRT 208
Wnt-10a GFGERFSKDFLDSREP-----HRDIHARMRLHNNRVGRQAVMENMR 260
Wnt-10b DFGKFSRDFLDSREA-----PRDIQARMRLHNNRVGRQVVTENLKR 245
Wnt-11 SYGLLMGAKFSDAPMKVKTG----SQANKMLRLHNSEVGRQALRASLEM 207
Wnt-16 QYGMWFSRKFLDFPIGNTT---GKENKVLLAMNLHNNNEAGRQAVAKLMSV 219

Wnt-1 ECKCHGMSGSCTVRTCWMRLPTLRAVG DVLRDRFDGASRVLYGNRGSNRA 266
Wnt-2 ECKCHGVSGSCTLRTCW LAMADFRKTGDYLRKYNGAIQVVMNQ---DGT 251
Wnt-2b ECKCHGVSGSCTLRTCW RALSDFRRTGDYLR RRYDGAVQVMATQ---DGA 263
Wnt-3 KCKCHGLSGSCEVKT CWWAQPDFRAIGDFLKD KYDSASEMVVEK---HRE 251
Wnt-3a KCKCHGLSGSCEVKT CWSQPDFAIGDFLKD KYDSASEMVVEK---HRE 248
Wnt-4 ECKCHGVSGSCEVKT CWRAPFPFRQVGHALKEKFDGATEVEPRR---VGS 251
Wnt-5a ACKCHGVSGSCLKTCWLQLADFRKVG DALKKEYDSAAAMRLNS---RCK 283
Wnt-5b ACKCHGVSGSCLKTCWLQLAEFRKVG DRLKEKYDSAAAMRVTR---KGR 262
Wnt-6 ECKCHGLSGSCALRTCWQKLPPFREVGA RLLERFHGASRVMGTN---DGK 267
Wnt-7a ECKCHGVSGSCTTKTCWTTLPQFRELGYVLKD KYNEAVHVEFVR---ASR 245
Wnt-7b ECKCHGVSGSCTTKTCWTTLPKFREVGHLLKEKYNAAVQVEVVR---ASR 245
Wnt-8a TCKCHGISGSCSIQT CWLQLAEFREMGDYLKAKYDQALKIEMDKRQ--LR 226
Wnt-8 TCKCHGVSGSCTTQTCWLQLPEFREVG AHLKEKYHAALKVDLLQG----- 223
Wnt-9a TCKCHGVSGSCTVRTCWRQLAPFHEVG KHLKHXYETALKVGSTTNEAAGE 263
Wnt-9b TCKCHGVSGSCAVRTCWKQLSPFRETGQV LKLRYDSAVKVSSATNEALGR 258
Wnt-10a KCKCHGTSGSCQLKTCWQVTPFRTV GALLRSRFHRATLIRPHNR--NGG 308
Wnt-10b KCKCHGTSGSCQFKTCWRAAPEFRAVGA ALRERLGRAIFIDTHNR--NSG 293
Wnt-11 KCKCHGVSGSCSIRTCWKG LQELQDVAADLKTRYLSATKVVHRP---MGT 254
Wnt-16 DCRCHGVSGSCAVKTCWKTMSSFEKIGHLL LDKYENSIQISDKT---KRK 266

Wnt-1 SRAELLR-----LEPEDPAHKPPSPHDLVYFEKSPNFCTYSGRLGTAGTA 311
Wnt-2 GFTVAN-----ERFKKPTKNDLVYFENS PDYICIRDREAGSLGTA 290
Wnt-2b NFTAAR-----QGYRRATRDLVYFDNS PDYCVLDKAAGSLGTA 302
Wnt-3 SRGWVET-----LRKYSLFKPPTERDLVYY ENSPNFCEPNPETGSFGTR 296
Wnt-3a SRGWVET-----LRPRYTYFKVPTERDLVYYE ASPNFCEPNPETGSFGTR 293
Wnt-4 SR----A-----LVPRNAQFKPHTDEDLVY LEPSPDFCEQDMRSGVLGTR 292
Wnt-5a -LVQVN-----SRFNSPTTQDLVYIDPS PDYCVRNES TGSLGTQ 321
Wnt-5b -LELVN-----SRFTQPTPEDLVYVDPSP DYCLRNES TGSLGTQ 300
Wnt-6 ALLPAVR-----TLKPPGRADLLYAADSP DFCAPNRRTGSPGTR 306
Wnt-7a NKRPFTFL-----KIKKPLSYRKPMDTDLVY IEKSPNYCEEDPVTGSGVTQ 290
Wnt-7b LRQPTFL-----RIKQLRSYQKPMETDLVY IEKSPNYCEEDAATGSGVTQ 290
Wnt-8a AGNSAEG-----HWVPAAEFLPSAAEALIF LEESPDYCTCNSSLGIYGE 271
Wnt-8 AGNSAAG-----RGAIADTFISISTREL VHLEDSPDYCLENKTLGLLGTE 268

FIG. 1 (Continued)

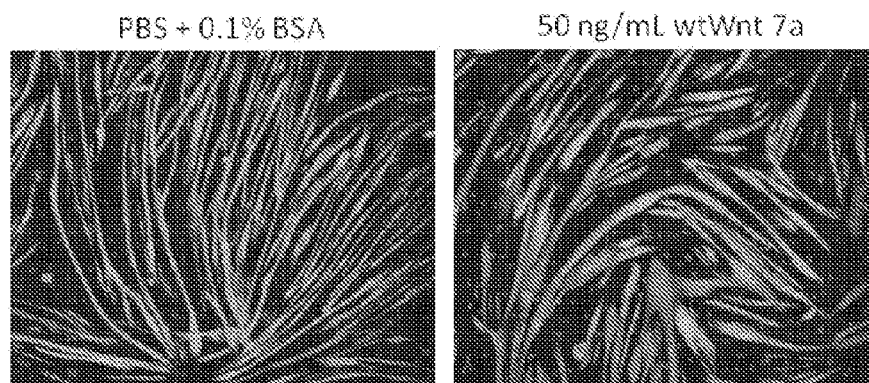
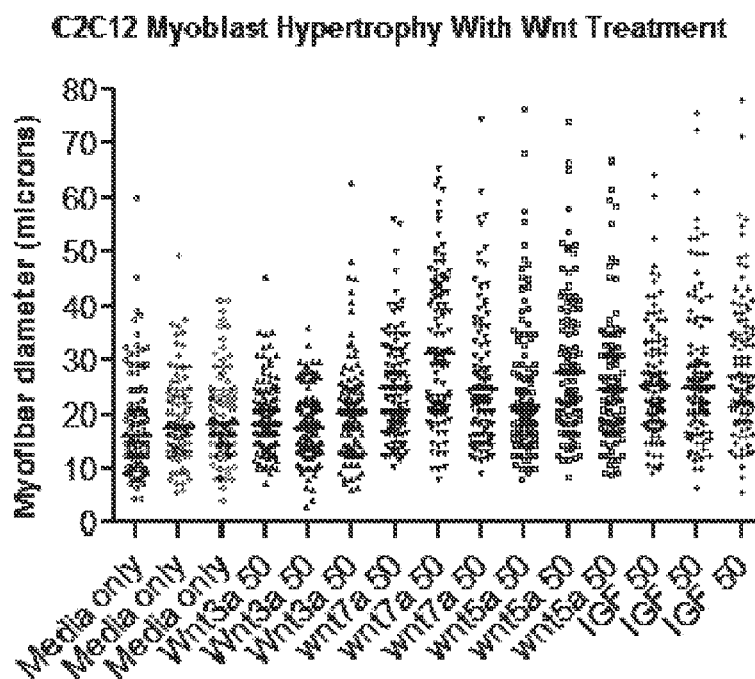
Wnt-9a	AGAISPPRGR--ASCAGGSDFLPRTPELVHLLDDSPSFCLAGR--FSPGTA	309
Wnt-9b	LELWAPAR-----QGSITKGLAPRSGDLVYMEDSPSFCRPSK--YSPGTA	301
Wnt-10a	QLEPGPAGAPSPAPGAPGPRRRASPADLVYFEKSPDFCEREPRLDAGTV	358
Wnt-10b	AFQPRLR-----PRRLSG--ELVYFEKSPDFCERDPTMGSPGTR	330
Wnt-11	RKHLVPK-----DLDIRPVKDSELYLQSSPDFCMKNEKVGSHGTQ	295
Wnt-16	MRR-----REKDQRKIPHKD-DLLVYNKSPNYCVEDKKLGIPGTQ	306
Wnt-1	GRACNSSSPALDGCELLCCGRGHRTRTQRVTER-----CNCTFHWCC	354
Wnt-2	GRVCNLTSGMDSCEVMCCGRGYDTSHTVTRMTK-----CGCKFHWCCA	333
Wnt-2b	GRVCSKTSKGTGCEIMCCGRGYDTTRVTRVTQ-----CECKFHWCCA	345
Wnt-3	DRTCNVTSHGIDGCDLLCCGRGHNRTEKRKEK-----CHCIFHWCCY	339
Wnt-3a	DRTCNVSSHGIDGCDLLCCGRGHNRARAERRREK-----CRCVFHWCCY	336
Wnt-4	GRTCNKTSKAIDGCELLCCGRGFHTAQVELAER-----CSCKFHWCCF	335
Wnt-5a	GRLCNKTSEGMDGCELMCCGRGYDQFKTVQTER-----CHCKFHWCCY	364
Wnt-5b	GRLCNKTSEGMDGCELMCCGRGYNQFKSVQVER-----CHCKFHWCCF	343
Wnt-6	GRACNSSAPDLSGCDLLCCGRGHRQESVQLEEN-----CLCRFHWCCV	349
Wnt-7a	GRACNKTAPOASGCDLMCCGRGYNTHQYARVWQ-----CNCKFHWCCY	333
Wnt-7b	GRLCNRTSPGADGCDTMCCGRGYNTHQYTKVWQ-----CNCKFHWCCF	333
Wnt-8a	GRECLQNSHNTSRWERRSCGRLCTEGLQVEERKTEVISSCNCKFQWCC	321
Wnt-8	GRECLRRGRALGRWERRSCRRLCGDCGLAVEERRAETVSSCNCKFHWCCA	318
Wnt-9a	GRRCHREK-----NCESICCGRGHNTQSRVTRP-----CQCQVRWCCY	348
Wnt-9b	GRVCSREA-----SCSSLCCGRGYDTQSRVAFS-----CHCQVQWCCY	340
Wnt-10a	GRLCNKSSAGSDGCGSMCCGRGHNILRQTRSER-----CHCRFHWCCF	401
Wnt-10b	GRACNKTSRLLDGCGSLCCGRGHNVLRQTRVER-----CHCRFHWCCY	373
Wnt-11	DRQCNKTSNGSDSCDLCCGRGYNPYTDREVVER-----CHCKYHWCCY	338
Wnt-16	GRECNRTSEGADGCNLLCCGRGYNTHVVRHVER-----CECKFIWCCY	349
Wnt-1	VSCRNCTHTRVLHECL-----	370
Wnt-2	VRCQDCLEALDVHTCKAPKNADWTTAT-----	360
Wnt-2b	VRCKECRNTVDVHTCKAPKKAEWLDQT-----	372
Wnt-3	VSCQECIRIYDVHTCK-----	355
Wnt-3a	VSCQECTRVYDVHTCK-----	352
Wnt-4	VKCRQCQRLVELHTCR-----	351
Wnt-5a	VKCKKCTEIVDQFVCK-----	380
Wnt-5b	VRCKKCTEIVDQYICK-----	359
Wnt-6	VQCHRCRVRKELSLCL-----	365
Wnt-7a	VKCNTCSERTEMYTCK-----	349
Wnt-7b	VKCNTCSERTEVFTCK-----	349
Wnt-8a	VKCDQCRHVVSKEYCARSP----GSAQSLGKGS	351
Wnt-8	VRCEQCRRRVTKYFCSRAERPRGGAHKPGRKP-	351
Wnt-9a	VECRQCTQREEVYTCKG-----	365
Wnt-9b	VECQOCVQEEELVYTCKH-----	357
Wnt-10a	VVCEECRITENVSVC-----	417
Wnt-10b	VLCDECKVTEWVNVCK-----	389
Wnt-11	VTCRRCERTVERYVCK-----	354
Wnt-16	VRCRRCESMTDVHTCK-----	365

FIG. 1 (Continued)

Wnt-7A Alignment

	10	20	30	40	50	60	70	80	
1	MNRKARRCLGHLFSLGLMVYLRIGGFSSVVALGASII	CNKIPGLAPRQRAICQSRPDAT	IIVIGEGSQMGLDECQFQFRNG	Wnt7A_Human					
1	MTRKARRCLGHLFSLGLIVYLRIGGFSSVVALGASII	CNKIPGLAPRQRAICQSRPDAT	IIVIGEGSQMGLDECQFQFRNG	Wnt7A_Mouse					
1	MTRKARRCLGHLFSLGLIVYLRIGGFSSVVALGASII	CNKIPGLAPRQRAICQSRPDAT	IIVIGEGSQMGLDECQFQFRNG	Wnt7A_Rat					
1	MNRKTRRWIFHIFLFLGLIVYLRIGGFSSVVALGASII	CNKIPGLAPRQRAICQSRPDAT	IIVIGEGSQMGINECCQFQFRNG	Wnt7A_Chicken					
1	MSRKTRRWIFHIFLFLGLIYLRIGGFSSVVALGASII	CNKIPGLAPRQRTICQSRPDAT	IIVIGEGAQMGINECCQFQFRNG	Wnt7A_Zebrafish					
1	MNRKARRCLGHLFSLGLIVYLRIGGFSSVVALGASII	CNKIPGLAPRQRAICQSRPDAT	IIVIGEGSQMGLDECQFQFRNG	Wnt7A_Pig					
1	MNRKARRCLGHLFSLGLMVYLRIGGFSSVVALGASII	CNKIPGLAPRQRAICQSRPDAT	IIVIGEGSQMGLDECQFQFRNG	Wnt7A_Cow					
	90	100	110	120	130	140	150	160	
81	RWNCSALGERTVFGKELKVGSR	EAAFTYAI	IAAGVAHAITAACTQGNLSDCGCDKEKQ	QYHRDEGWKGGCSADIRYGI	Wnt7A_Human				
81	RWNCSALGERTVFGKELKVGSR	EAAFTYAI	IAAGVAHAITAACTQGNLSDCGCDKEKQ	QYHRDEGWKGGCSADIRYGI	Wnt7A_Mouse				
81	RWNCSALGERTVFGKELKVGSR	EAAFTYAI	IAAGVAHAITAACTQGNLSDCGCDKEKQ	QYHRDEGWKGGCSADIRYGI	Wnt7A_Rat				
81	RWNCSALGERTVFGKELKVGSR	EAAFTYAI	IAAGVAHAITAACTQGNLSDCGCDKEKQ	QYHKEEGWKGGCSADIRYGI	Wnt7A_Chicken				
81	RWNCSALGERTVFGKELKVGSR	EAAFTYAI	IAAGVAHAITAACTQGNLSDCGCDKEKQ	QGFYNQDEGWKGGCSADIRYGL	Wnt7A_Zebrafish				
81	RWNCSALGERTVFGKELKVGSR	EAAFTYAI	IAAGVAHAITAACTQGNLSDCGCDKEKQ	QYHRDEGWKGGCSADIRYGI	Wnt7A_Pig				
81	RWNCSALGERTVFGKELKVGSR	EAAFTYAI	IAAGVAHAITAACTQGNLSDCGCDKEKQ	QYHRDEGWKGGCSADIRYGI	Wnt7A_Cow				
	170	180	190	200	210	220	230	240	
161	GF	AKV	FVDAREIKQ	NARTLMNLHNNHNEAGRKILEENMKLECKCHGVSGSCTT	TKCWTTLQFRELGYVLKDKYNEAVHVEP	Wnt7A_Human			
161	GF	AKV	FVDAREIKQ	NARTLMNLHNNHNEAGRKILEENMKLECKCHGVSGSCTT	TKCWTTLQFRELGYVLKDKYNEAVHVEP	Wnt7A_Mouse			
161	GF	AKV	FVDAREIKQ	NARTLMNLHNNHNEAGRKILEENMKLECKCHGVSGSCTT	TKCWTTLQFRELGYVLKDKYNEAVHVEP	Wnt7A_Rat			
161	GF	AKV	FVDAREIKQ	NARTLMNLHNNHNEAGRKILEENMKLECKCHGVSGSCTT	TKCWTTLQFRELGYVLKDKYNEAVHVEP	Wnt7A_Chicken			
161	3	FSK	VFLDAREIKQ	NARTLMNLHNNHNEAGRKILEENMKLECKCHGVSGSCTT	TKCWTTLQFRELGYVLKDKYNEAVHVEP	Wnt7A_Zebrafish			
161	GF	AKV	FVDAREIKQ	NARTLMNLHNNHNEAGRKILEENMKLECKCHGVSGSCTT	TKCWTTLQFRELGYVLKDKYNEAVHVEP	Wnt7A_Pig			
161	GF	AKV	FVDAREIKQ	NARTLMNLHNNHNEAGRKILEENMKLECKCHGVSGSCTT	TKCWTTLQFRELGYVLKDKYNEAVHVEP	Wnt7A_Cow			
	250	260	270	280	290	300	310	320	
241	VR	ASR	NKRPTFLKIKKPLSYRKPM	DTDLVYIEKSPNYCEEDPVTG	SVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR	Wnt7A_Human			
241	VR	ASR	NKRPTFLKIKKPLSYRKPM	DTDLVYIEKSPNYCEEDPVTG	SVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR	Wnt7A_Mouse			
241	VR	ASR	NKRPTFLKIKKPLSYRKPM	DTDLVYIEKSPNYCEEDPVTG	SVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR	Wnt7A_Rat			
241	VR	ASR	NKRPTFLKIKKPLSYRKPM	DTDLVYIEKSPNYCEEDPVTG	SVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR	Wnt7A_Chicken			
241	VR	ASR	NKRPTFLKIKKPLSYRKPM	DTDLVYIEKSPNYCEADPVTG	SMGTQGRICNKTAPQHTNGCDLMCCGRGYNTHQYSR	Wnt7A_Zebrafish			
241	VR	ASR	NKRPTFLKIKKPLSYRKPM	DTDLVYIEKSPNYCEEDPVTG	SVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR	Wnt7A_Pig			
241	VR	ASR	NKRPTFLKIKKPLSYRKPM	DTDLVYIEKSPNYCEEDPATG	SVGTQGRACNKTAPQASGCDLMCCGRGYNTHQYAR	Wnt7A_Cow			
	330	340							
321	VQ	QCN	KPFHWCCYVKNTCS	ERT	EMYTCK	Wnt7A_Human			
321	VQ	QCN	KPFHWCCYVKNTCS	ERT	EMYTCK	Wnt7A_Mouse			
321	VQ	QCN	KPFHWCCYVKNTCS	ERT	EMYTCK	Wnt7A_Rat			
321	VQ	QCN	KPFHWCCYVKNTCS	ERT	EVYTCK	Wnt7A_Chicken			
321	VQ	QCN	KPLWCCYVKNTCS	ERT	EVYTCK	Wnt7A_Zebrafish			
321	VQ	QCN	KPFHWCCYVKNTCS	ERT	EVYTCK	Wnt7A_Pig			
321	VQ	QCN	KPFHWCCYVKNTCS	ERT	EVYTCK	Wnt7A_Cow			

FIG. 2

*FIG. 3A**FIG. 3B*

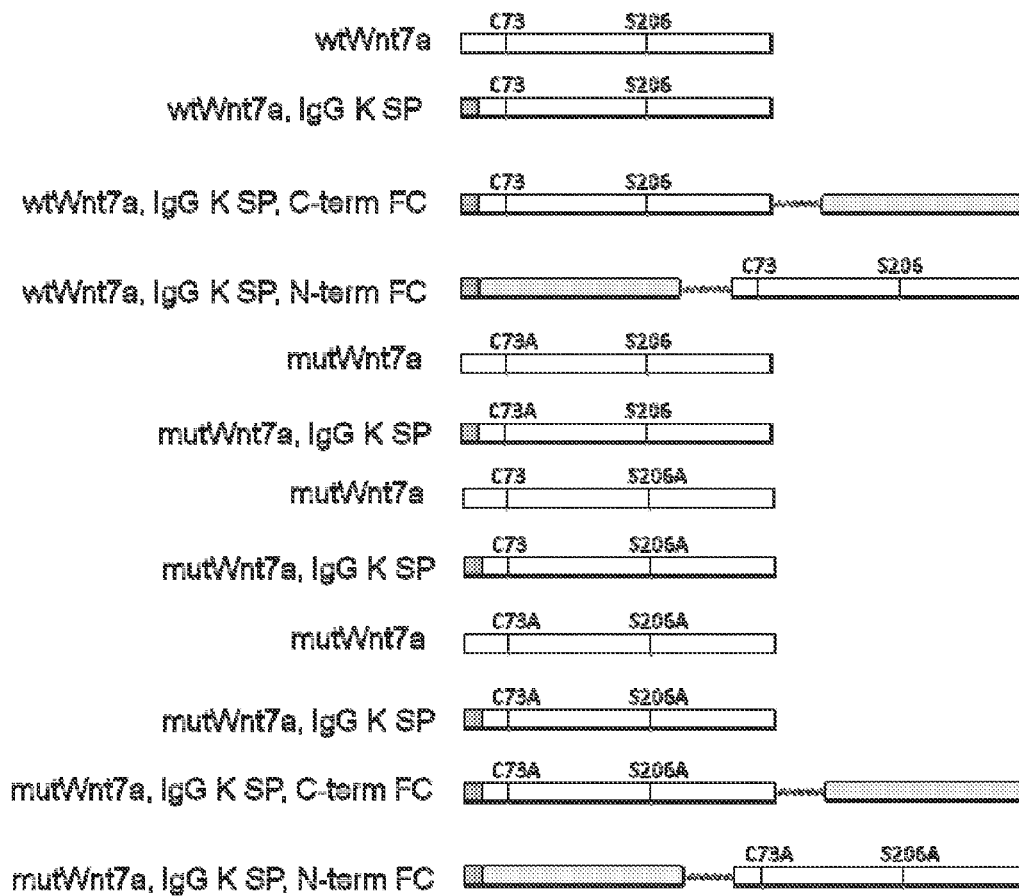


FIG. 4

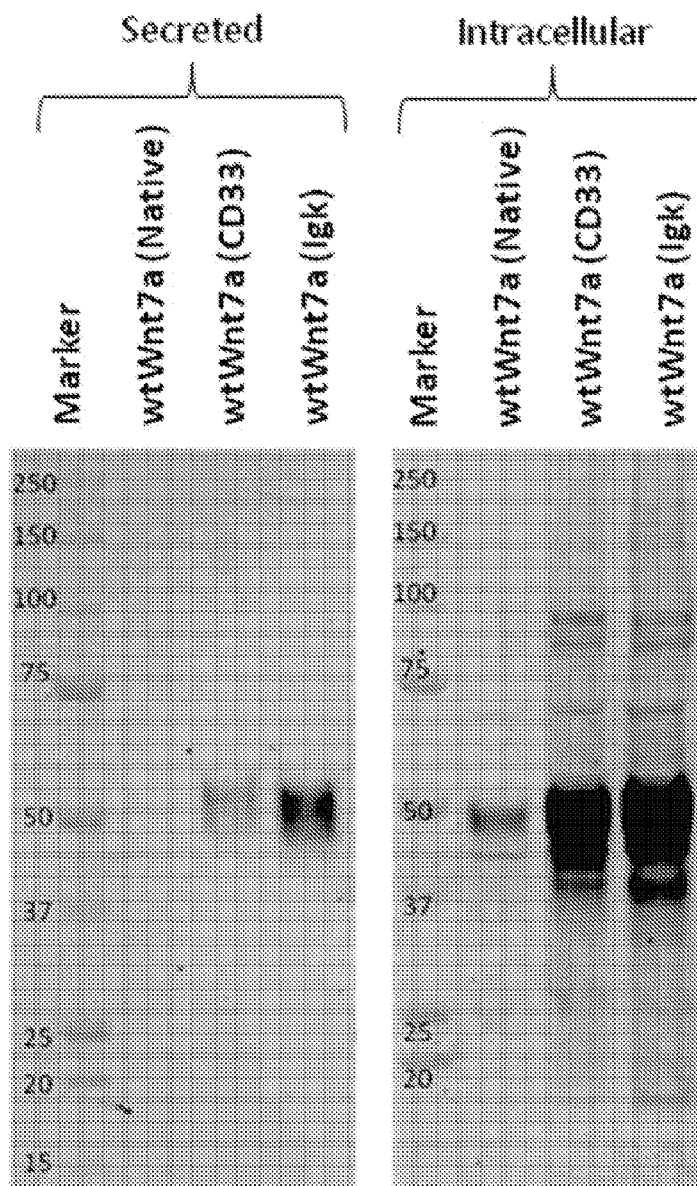


FIG. 5

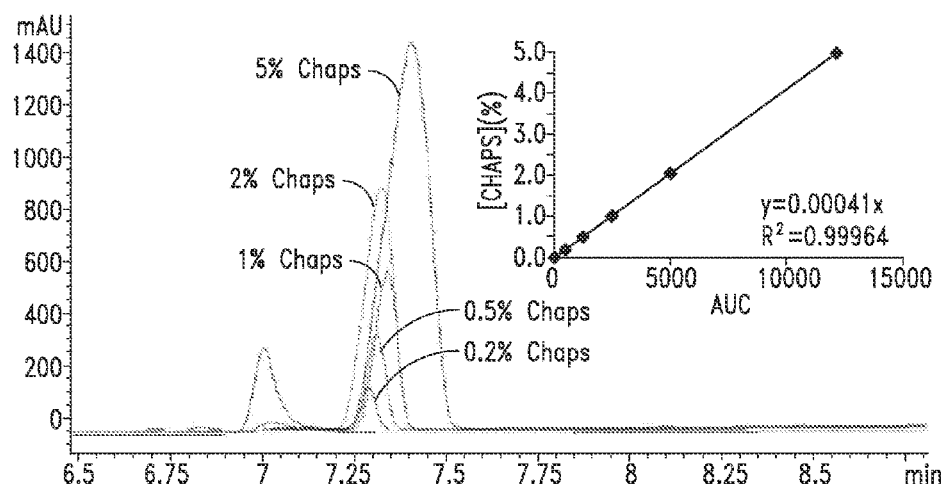


FIG. 6A

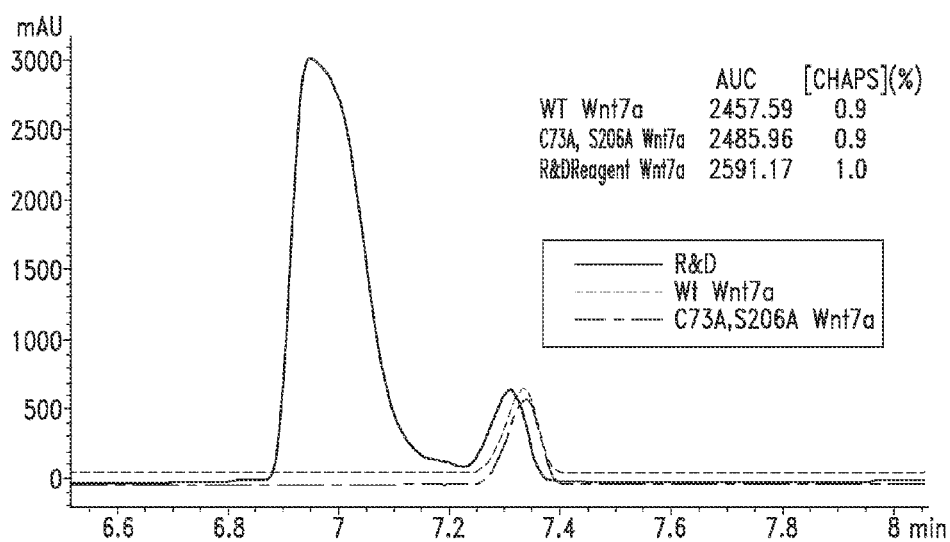
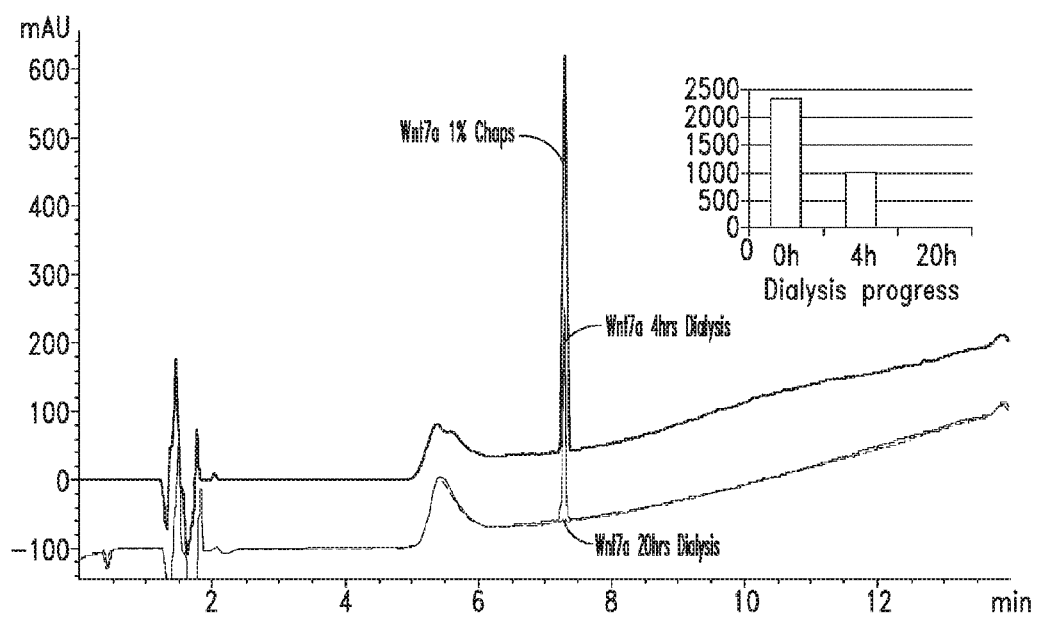
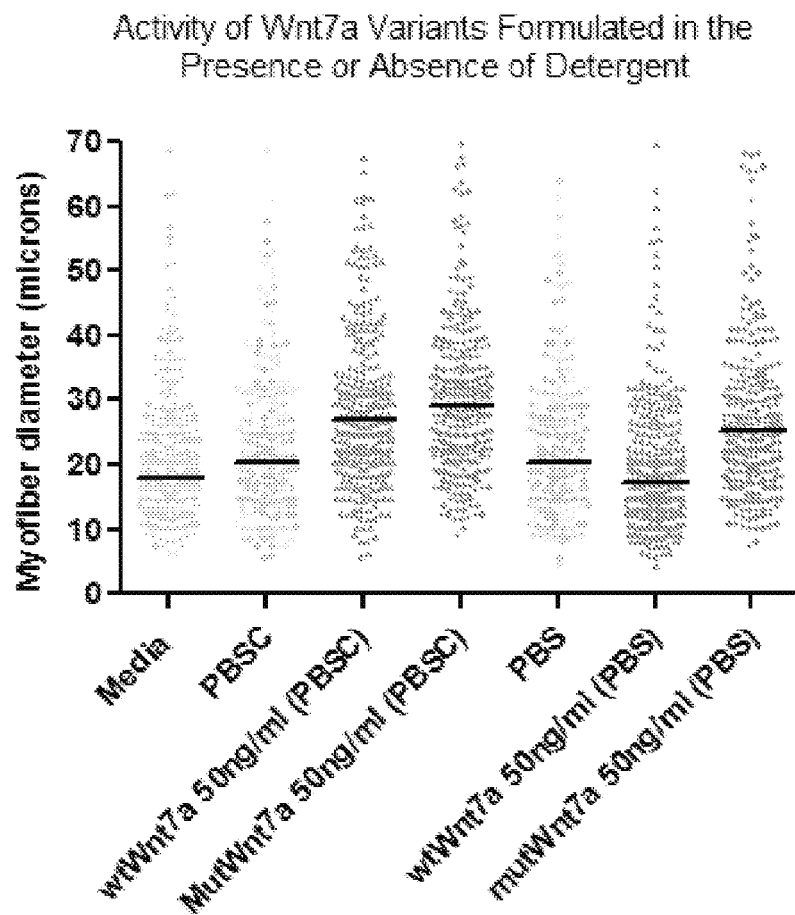


FIG. 6B

*FIG. 6C*

*FIG. 7*

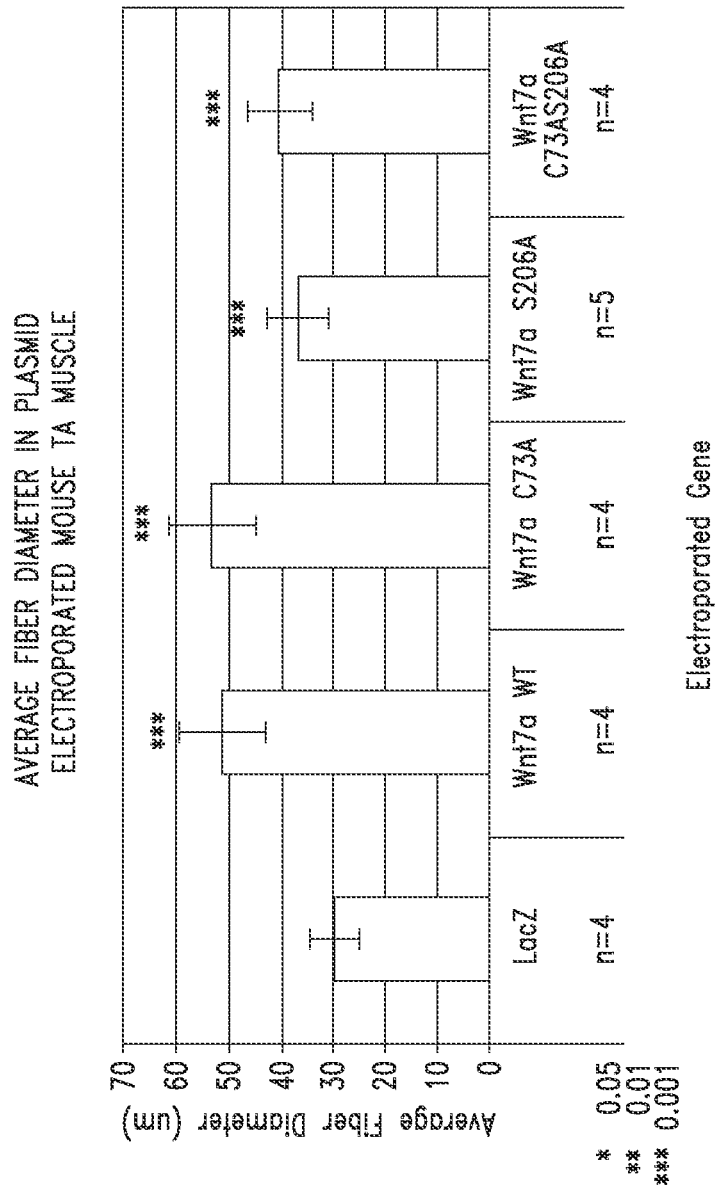


FIG. 8

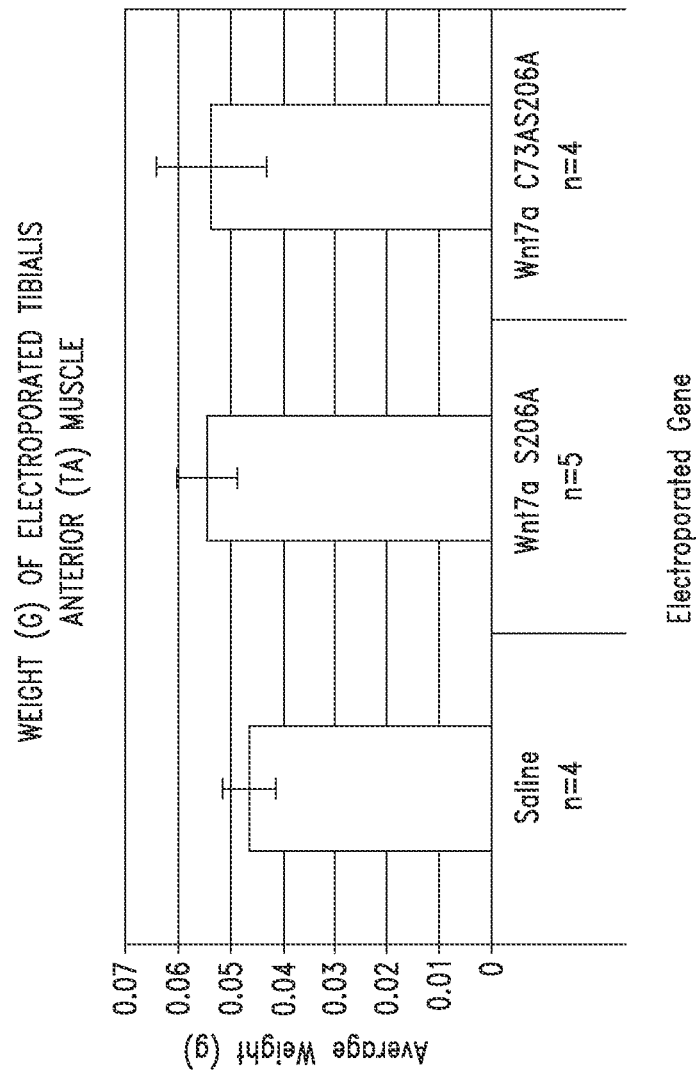


FIG. 9

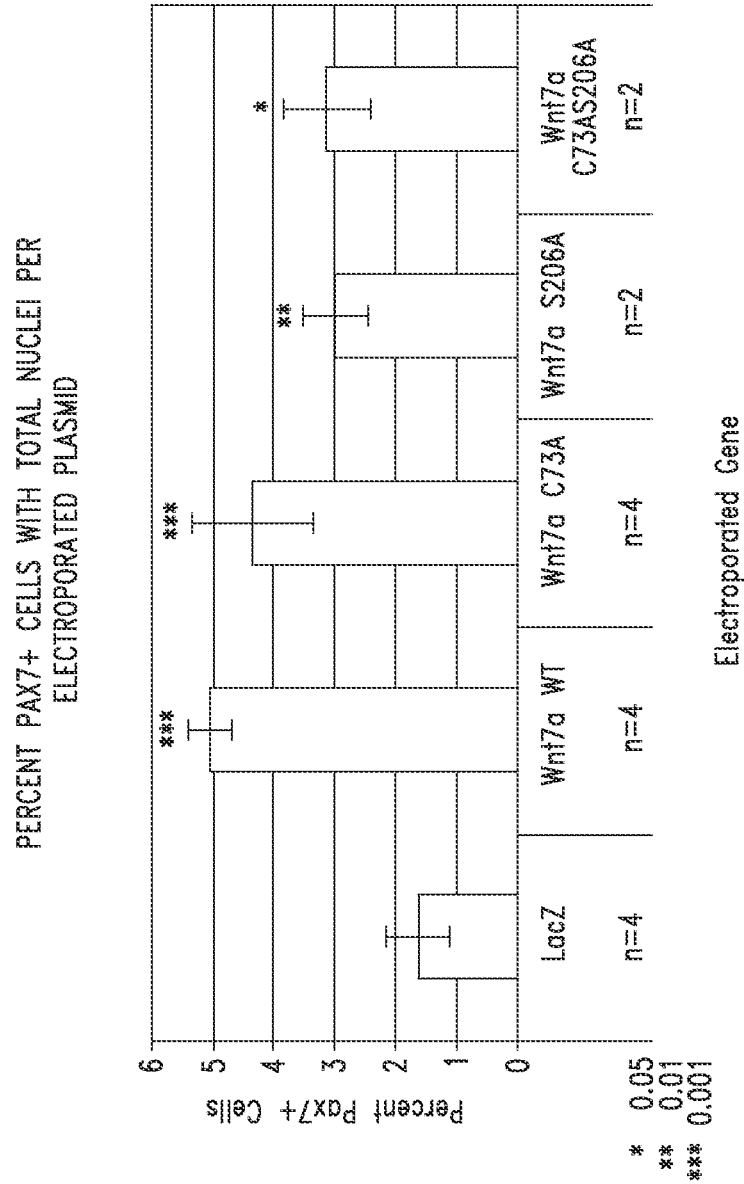
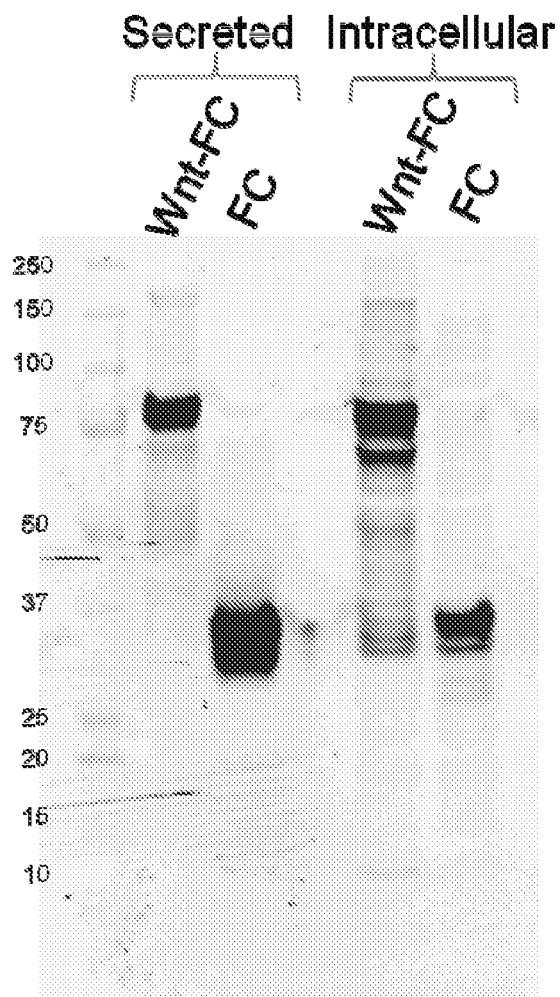
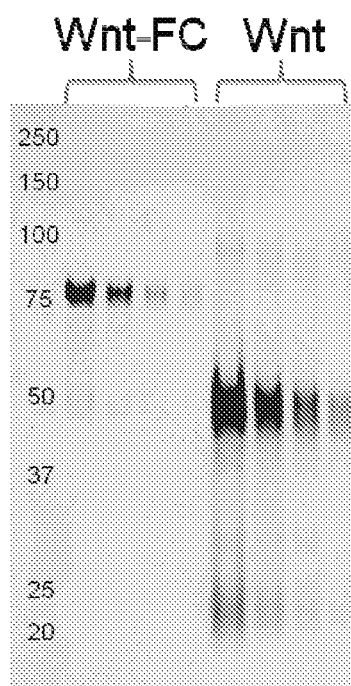


FIG. 10

*FIG. 11A*

*FIG. 11B*

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WNT COMPOSITIONS AND THERAPEUTIC USES OF SUCH COMPOSITIONS

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a U.S. national phase of PCT/US2012/020984, filed Jan. 11, 2012, which application claims the benefit under 35 U.S.C. §119(e) of U.S. Provisional Application No. 61/431,701, filed Jan. 11, 2012, each of which is incorporated by reference herein, in its entirety.

STATEMENT REGARDING SEQUENCE LISTING

The Sequence Listing associated with this application is provided in text format in lieu of a paper copy, and is hereby incorporated by reference into the specification. The name of the text file containing the Sequence Listing is FATE_095_00WO_ST25.txt. The text file is 124 KB, was created on Jan. 11, 2011, and is being submitted electronically via EFS-Web.

BACKGROUND

1. Technical Field

The invention relates generally to novel Wnt compositions and therapeutic methods of using the same. The Wnt polypeptides of the invention and compositions thereof may be used therapeutically, for example for promoting muscle regeneration by promoting stem cell expansion and muscle hypertrophy.

2. Description of the Related Art

The Wnt family of genes encodes over twenty cysteine-rich, secreted Wnt glycoproteins that act by binding to Frizzled (Fzd) receptors on target cells. Frizzled receptors are a family of G-protein coupled receptor proteins. Binding of different members of the Wnt-family to certain members of the Fzd family can initiate signaling by one of several distinct pathways. In the “canonical pathway,” activation of the signaling molecule, Disheveled, leads to the inactivation of glycogen synthase kinase-3 (GSK-3 β), a cytoplasmic serine-threonine kinase. The GSK-3 β target, β -catenin, is thereby stabilized and translocates to the nucleus where it activates TCF (T-cell-factor)-dependant transcription of specific promoters (Wodarz, 1998, Dierick, 1999). “Non-canonical” Wnt pathway activation includes a subset of interactions between Wnt and Fzd that may activate Ca²⁺ pathway signaling and potentially PI3K signaling, Rho pathway signaling, and planar cell polarity (PCP) pathway signaling.

Wnts are secreted glycoproteins that function as paracrine or autocrine signals active in several primitive cell types. Although Wnt proteins are secreted from cells, they are found to be hydrophobic and are post-translationally modified by addition of a lipid moiety at a conserved cysteine residue and a conserved serine residue. These lipid modifications are widely accepted to be important for the biological activity and secretion of Wnt proteins. Lipidation and the low solubility of lipidated Wnts, however, are associated with low production yields when detergents are not used during formulation and thus, present a unique challenge for clinical scale production of Wnt. Thus, while Wnts have a tremendous potential for use as therapeutics in a variety of clinical settings, the therapeutic potential of Wnts has yet to be fully realized due to Wnt insolubility and corresponding insufficient production as a purified, biologically active therapeutic.

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Accordingly, the art is in need of soluble, novel Wnt polypeptides that retain Wnt biological activity, methods for generating the novel Wnts on a clinical scale, and methods of using the novel Wnts to promote tissue formation, regeneration, maintenance and repair.

BRIEF SUMMARY

The invention provides modified Wnt polypeptides comprising one or more amino acids that reduce lipidation of the Wnt polypeptide. In a particular embodiment, the Wnt polypeptide comprises one or more amino acid deletions, insertions, or substitutions that reduce lipidation of the Wnt polypeptide.

In one embodiment, the polypeptide is a Wnt polypeptide that activates a non-canonical Wnt signaling pathway.

In a particular embodiment, a Wnt polypeptide that activates a non-canonical Wnt signaling pathway is selected from the group consisting of: Wnt4, Wnt5a, Wnt5b, Wnt6, Wnt7a, Wnt7b, and Wnt11.

In some embodiments of the invention, the polypeptide is a Wnt7a or Wnt 5a polypeptide.

In particular embodiments, the invention provides a modified Wnt7a polypeptide having decreased lipidation relative to the lipidation of the Wnt7a polypeptide corresponding to any one of SEQ ID NOs: 2 and 6-11. In other embodiments, the invention provides a modified Wnt7a polypeptide comprising an amino acid deletion, insertion, or substitution at the amino acid position corresponding to position 73 of any one of SEQ ID NOs: 2 and 6-11. In some embodiments, the invention provides a Wnt7a polypeptide comprising an amino acid deletion, insertion, or substitution at the amino acid position corresponding to position 206 of any one of SEQ ID NOs: 2 and 6-11. In particular embodiments, the invention provides a Wnt7a polypeptide comprising amino acid deletions, insertions, or substitutions at the amino acid positions corresponding to positions 73 and 206 of any one of SEQ ID NOs: 2 and 6-11.

In some embodiments, the invention provides a Wnt7a polypeptide comprising an Alanine at the amino acid position corresponding to position 73 or 206 of any one of SEQ ID NOs: 2 and 6-11. In other embodiments, the invention provides a Wnt7a polypeptide comprising Alanine at the amino acid positions corresponding to positions 73 and 206 of any one of SEQ ID NOs: 2 and 6-11. The invention also provides a composition comprising any of the embodiments herein wherein the Wnt7a polypeptide is a human or mouse Wnt7a polypeptide.

In particular embodiments, the invention provides a modified Wnt5a polypeptide having decreased lipidation relative to the lipidation of the Wnt5a polypeptide corresponding to any one of SEQ ID NOs: 15 and 19-23. In other embodiments, the invention provides a modified Wnt5a polypeptide comprising an amino acid deletion, insertion, or substitution at the amino acid position corresponding to position 104 of any one of SEQ ID NOs: 15 and 19-23. In some embodiments, the invention provides a Wnt5a polypeptide comprising an amino acid deletion, insertion, or substitution at the amino acid position corresponding to position 244 of any one of SEQ ID NOs: 15 and 19-23. In particular embodiments, the invention provides a Wnt5a polypeptide comprising amino acid deletions, insertions, or substitutions at the amino acid positions corresponding to positions 104 and 244 of any one of SEQ ID NOs: 15 and 19-23.

In some embodiments, the invention provides a Wnt5a polypeptide comprising an Alanine at the amino acid position corresponding to position 104 or 244 of any one of SEQ ID

NOs: 15 and 19-11. In other embodiments, the invention provides a Wnt5a polypeptide comprising Alanine at the amino acid positions corresponding to positions 104 and 244 of any one of SEQ ID NOs: 15 and 19-23. The invention also provides a composition comprising any of the embodiments herein wherein the Wnt5a polypeptide is a human or mouse Wnt5a polypeptide.

In some embodiments, the invention provides a Wnt polypeptide comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 3-5, 12-13, and 16-18.

In various embodiments, the present invention contemplates, in part, a fusion polypeptide comprising a Wnt polypeptide comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 3-5, 12-13, and 16-18.

In one embodiment, the fusion polypeptide comprises a native signal peptide, a heterologous signal peptide, or a hybrid of a native and a heterologous signal peptide.

In a particular embodiment, the heterologous signal peptide is selected from the group consisting of: a CD33 signal peptide, an immunoglobulin signal peptide, a growth hormone signal peptide, an erythropoietin signal peptide, an albumin signal peptide, a secreted alkaline phosphatase signal peptide, and a viral signal peptide.

In a certain embodiment, the heterologous signal peptide is a CD33 signal peptide, an IgGκ signal peptide, or an IgGμ signal peptide.

In additional embodiments, the fusion polypeptide comprises a heterologous protease cleavage site.

In one embodiment, the heterologous protease cleavage site is selected from the group consisting of: a tobacco etch virus (TEV) protease cleavage site, a heparin cleavage site, a thrombin cleavage site, an enterokinase cleavage site and a Factor Xa cleavage site.

In further embodiments, the fusion polypeptide comprises an epitope tag selected from the group consisting of: a HIS6 epitope, a MYC epitope, a FLAG epitope, a V5 epitope, a VSV-G epitope, and an HA epitope.

In particular embodiments, the fusion polypeptide comprises an amino acid sequence as set forth in any one of SEQ ID NOs: 3-5 and 12-13, has increased production, secretion, or solubility compared to a corresponding native Wnt polypeptide as set forth in SEQ ID NOs: 2 and 6-11.

In certain embodiments, the fusion polypeptide comprises an amino acid sequence as set forth in any one of SEQ ID NOs: 16-18, has increased production, secretion, or solubility compared to a corresponding native Wnt polypeptide as set forth in SEQ ID NOs: 15 and 19-23.

The invention also provides polynucleotides encoding Wnt polypeptides having one or more amino acids that reduce lipidation of the Wnt polypeptide. Some embodiments of the invention provide a vector comprising a polynucleotide encoding a Wnt polypeptide having one or more amino acids that reduce lipidation of the Wnt polypeptide. The invention also provides a host cell comprising such vector, and Wnt polypeptides produced by the host cell.

The invention also provides compositions comprising the Wnt polypeptides, polynucleotides, and vectors of the invention. In some embodiments, the composition comprises a pharmaceutically-acceptable salt, carrier, or excipient, and in some embodiments, the composition is soluble in an aqueous solution. In particular embodiments of the invention, the composition is formulated for injection. In certain embodiments, the composition is formulated without a detergent. In related embodiments, detergent is substantially absent from the formulation of the composition. In another related embodiment, the formulated composition is substantially free of detergent. In more specific embodiments the composition

is formulated for one or more of intravenous injection, intracardiac injection, subcutaneous injection, intraperitoneal injection, or direct injection into a muscle.

In some embodiments of the invention, the composition promotes tissue formation, regeneration, maintenance or repair. In particular embodiments, the tissue is muscle, and in more specific embodiments the muscle is skeletal, cardiac, or smooth muscle.

In other embodiments, the composition of the invention promotes stem cell expansion. In some embodiments, the stem cell is an adult stem cell, and in particular embodiments, the adult stem cell is a satellite stem cell.

In some embodiments, the composition of the invention promotes muscle hypertrophy or prevents atrophy.

The invention additionally provides a method for treating or preventing muscle loss comprising administering to a subject a composition having a Wnt polypeptide comprising one or more amino acids that reduce lipidation of the Wnt polypeptide. In some embodiments, the composition comprises a pharmaceutically-acceptable salt, carrier, or excipient, and in particular embodiments the composition is soluble in an aqueous solution. In other particular embodiments, the composition is formulated for injection, and in even more particular embodiments, the composition is formulated for one or more of intravenous injection, intracardiac injection, subcutaneous injection, intraperitoneal injection, or direct injection into muscle.

In certain embodiments, the composition is formulated without a detergent. In related embodiments, detergent is substantially absent from the formulation of the composition. In another related embodiment, the formulated composition is substantially free of detergent.

In some embodiments of the method of the invention, the subject has or is at risk of having a disease or condition affecting muscle. In particular embodiments, the disease is a degenerative disease, and in more particular embodiments the degenerative disease is muscular dystrophy. In even more particular embodiments, the muscular dystrophy is selected from Duchenne muscular dystrophy (DMD), Becker muscular dystrophy (BMD), Emery-Dreifuss muscular dystrophy, Landouzy-Dejerine muscular dystrophy, facioscapulo-humeral muscular dystrophy (FSH), Limb-Girdle muscular dystrophies, von Graefe-Fuchs muscular dystrophy, oculopharyngeal muscular dystrophy (OPMD), Myotonic dystrophy (Steinert's disease) and congenital muscular dystrophies.

In other embodiments of the method, the disease or condition affecting muscle is a wasting disease, muscular atrophy, muscle atrophy, ICU-induced weakness, prolonged disuse, surgery-induced weakness, or a muscle degenerative disease. In more particular embodiments, the condition is muscle atrophy associated with muscle disuse, immobilization, surgery-induced weakness, or injury.

In some embodiments, administering the composition promotes muscle atrophy. In particular embodiments, the muscle is skeletal muscle or cardiac muscle.

In other embodiments of the method of the invention, administering the composition promotes satellite cell expansion.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

FIG. 1 shows a ClustalW alignment of all 19 human Wnt polypeptide sequences. Conserved potential post-translational lipidation sites are shaded in grey and aligned with Cysteine 73 and Serine 206 of Human Wnt 7a. Asparagine residues thought to be sites of glycosylation are underlined.

FIG. 2 shows a ClustalW alignment of the conserved Wnt7a polypeptide sequences from various species.

FIG. 3 shows Myoblast hypertrophy on stimulation with non-canonical Wnts. FIG. 3a shows a representative image of in vitro myoblast hypertrophy stimulated by a non-canonical Wnt treatment (Wnt7a). FIG. 3b shows data of in vitro myoblast fiber hypertrophy induced by certain Wnt treatments. 100 fibers were counted for each of 3 biological replicates for each treatment group and individual counts in microns and replicate medians are displayed.

FIG. 4 shows a schematic representation of the various constructed Wnt7a variants. Wild type human Wnt7a sequence is shown in white, variants with specific point mutations leading to amino acid changes are seen in white with amino acid changes as indicated. Replacement of the naturally occurring Wnt7a secretion signal peptide with that of human IgG Kappa chain is indicated as grey shading. Amino or carboxy-terminal fusions of immunoglobulin Fc regions were constructed with linker regions as indicated.

FIG. 5 shows a SDS-PAGE, Western blot of Wnt7a expressed and secreted from HEK293 cells in mammalian tissue culture. The increased expression and subsequent secretion of Wnt polypeptides with exogenous secretion signal peptides from CD33 or IgG Kappa chain can be clearly seen over that of the native signal peptide.

FIG. 6 shows High Performance Liquid Chromatography (HPLC) traces detecting the detergent CHAPS in solution. FIG. 6a shows the standard curve for chaps in Phosphate Buffered Saline to calibrate the system. FIG. 6b shows preparations of modified Wnt polypeptides formulated in 1% CHAPS compared with the commercially available protein from R&D systems (the commercial protein contains a carrier protein that results in a second, larger peak). FIG. 6c shows the effective removal of CHAPS from the formulation of the Wnt polypeptides using dialysis over 4 and 20 hours as indicated.

FIG. 7 shows a myoblast hypertrophy assay displaying the activity of Wnt7a variants formulated in the presence or absence of detergent. Wnt proteins were constructed with the IgG Kappa secretion signal peptide. Proteins were produced in HEK293 mammalian culture systems and affinity purified. The proteins were formulated in PBS with 1% Chaps detergent. Aliquots of Each protein variant were reformulated by detergent removal using dialysis. Proteins were seen to have equal molar concentration and were applied to the C2C12 Hypertrophy assay.

FIG. 8 shows the results of an experiment to determine the average fiber diameter of mouse tibialis anterior (TA) muscles electroporated with expression plasmids encoding modified human Wnt7a polypeptides as discussed elsewhere herein, wild type human Wnt7a, or a LacZ control.

FIG. 9 shows the results of an experiment to determine the weight of mouse tibialis anterior (TA) muscles electroporated with expression plasmids encoding modified human Wnt7a polypeptides as discussed elsewhere herein, or a saline control.

FIG. 10 shows the results of an experiment to determine the number of Pax7+ satellite stem cells in mouse tibialis anterior (TA) muscles electroporated with expression plasmids encoding modified human Wnt7a polypeptides as discussed elsewhere herein, wild type human Wnt7a, or a LacZ control.

FIG. 11 immunoglobulin Fc fusion proteins. FIG. 11a shows a western blot of a Wnt7a protein with its native secretion signal peptide replaced with the signal peptide from immunoglobulin Kappa and constructed as a immunoglobulin Fc domain fusion protein. The secretion from mammalian culture systems is shown in FIG. 11a in comparison to Fc

domain-alone control. FIG. 11b shows the relative molecular weight differences between Wnt7a and Wnt7a-Fc fusion protein by SDS-PAGE western blot using an anti-Wnt7a detection antibody.

BRIEF DESCRIPTION OF THE SEQUENCE IDENTIFIERS

SEQ ID NO: 1 sets forth a cDNA sequence of human Wnt7a.

SEQ ID NO: 2 sets forth the amino acid sequence of the human Wnt7a polypeptide encoded by SEQ ID NO: 1.

SEQ ID NO: 3 sets forth the amino acid sequence of the human Wnt7a polypeptide of SEQ ID NO: 2, having an alanine mutation at amino acid position 73.

SEQ ID NO: 4 sets forth the amino acid sequence of the human Wnt7a polypeptide of SEQ ID NO: 2, having an alanine mutation at amino acid position 206.

SEQ ID NO: 5 sets forth the amino acid sequence of the human Wnt7a polypeptide of SEQ ID NO: 2, having an alanine mutation at amino acid position 73 and at position 206.

SEQ ID NO: 6 sets forth the amino acid sequence of a mouse Wnt7a polypeptide.

SEQ ID NO: 7 sets forth the amino acid sequence of a rat Wnt7a polypeptide.

SEQ ID NO: 8 sets forth the amino acid sequence of a chicken Wnt7a polypeptide.

SEQ ID NO: 9 sets forth the amino acid sequence of a zebrafish Wnt7a polypeptide.

SEQ ID NO: 10 sets forth the amino acid sequence of a porcine Wnt7a polypeptide.

SEQ ID NO: 11 sets forth the amino acid sequence of a bovine Wnt7a polypeptide.

SEQ ID NO: 12 sets forth the amino acid sequence of a human Wnt7a polypeptide with the native secretion signal peptide replaced with the signal peptide of Human Immunoglobulin Kappa Chain.

SEQ ID NO: 13 sets forth the amino acid sequence of a human Wnt7a polypeptide having an alanine mutation at amino acid position 73 and at position 206, with the native secretion signal peptide replaced with the signal peptide of Human Immunoglobulin Kappa Chain.

SEQ ID NO: 14 sets forth a cDNA sequence of human Wnt5a.

SEQ ID NO: 15 sets forth the amino acid sequence of the human Wnt5a polypeptide encoded by SEQ ID NO: 14.

SEQ ID NO: 16 sets forth the amino acid sequence of the human Wnt5a polypeptide of SEQ ID NO: 15, having an alanine mutation at amino acid position 104.

SEQ ID NO: 17 sets forth the amino acid sequence of the human Wnt5a polypeptide of SEQ ID NO: 15, having an alanine mutation at amino acid position 244.

SEQ ID NO: 18 sets forth the amino acid sequence of the human Wnt5a polypeptide of SEQ ID NO: 15, having an alanine mutation at amino acid position 104 and at position 244.

SEQ ID NO: 19 sets forth the amino acid sequence of a mouse Wnt5a polypeptide.

SEQ ID NO: 20 sets forth the amino acid sequence of a rat Wnt5a polypeptide.

SEQ ID NO: 21 sets forth the amino acid sequence of a chicken Wnt5a polypeptide.

SEQ ID NO: 22 sets forth the amino acid sequence of a zebrafish Wnt5a polypeptide.

SEQ ID NO: 23 sets forth the amino acid sequence of a bovine Wnt5a polypeptide.

SEQ ID NO: 24 sets forth the amino acid sequence of a human Wnt1 polypeptide.

SEQ ID NO: 25 sets forth the amino acid sequence of a human Wnt2 polypeptide.

SEQ ID NO: 26 sets forth the amino acid sequence of a human Wnt2b polypeptide.

SEQ ID NO: 27 sets forth the amino acid sequence of a human Wnt3 polypeptide.

SEQ ID NO: 28 sets forth the amino acid sequence of a human Wnt3a polypeptide.

SEQ ID NO: 29 sets forth the amino acid sequence of a human Wnt4 polypeptide.

SEQ ID NO: 30 sets forth the amino acid sequence of a human Wnt5b polypeptide.

SEQ ID NO: 31 sets forth the amino acid sequence of a human Wnt6 polypeptide.

SEQ ID NO: 32 sets forth the amino acid sequence of a human Wnt7b polypeptide.

SEQ ID NO: 33 sets forth the amino acid sequence of a human Wnt8a polypeptide.

SEQ ID NO: 34 sets forth the amino acid sequence of a human Wnt8b polypeptide.

SEQ ID NO: 35 sets forth the amino acid sequence of a human Wnt9a polypeptide.

SEQ ID NO: 36 sets forth the amino acid sequence of a human Wnt9b polypeptide.

SEQ ID NO: 37 sets forth the amino acid sequence of a human Wnt10a polypeptide.

SEQ ID NO: 38 sets forth the amino acid sequence of a human Wnt10b polypeptide.

SEQ ID NO: 39 sets forth the amino acid sequence of a human Wnt11 polypeptide.

SEQ ID NO: 40 sets forth the amino acid sequence of a human Wnt16 polypeptide.

SEQ ID NOs: 41-46 set forth oligonucleotide sequences.

DETAILED DESCRIPTION

A. Overview

While post-translational lipidation of Wnts is believed to be required for biological activity and protein secretion, the invention provides novel Wnt polypeptides having the amino acid sites of lipidation altered so that no post-translational lipidation occurs. The proteins of the invention retain Wnt biological activity, and the invention thus provides modified Wnt compositions having improved biologic drug-like properties such as enhanced solubility, production, and formulation, and therapeutic uses for such Wnt compositions. The invention provides a novel solution to the problem posed by the insolubility of Wnt polypeptides and further, provides inventive Wnt polypeptides, including fusion polypeptides, that are suitable for clinical scale production and therapeutic use. Therapeutic uses for the Wnt compositions of the invention include, for example, promoting tissue formation, regeneration, repair or maintenance.

The practice of the invention will employ, unless indicated specifically to the contrary, conventional methods of chemistry, biochemistry, organic chemistry, molecular biology, microbiology, recombinant DNA techniques, genetics, immunology, and cell biology that are within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, e.g., Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (3rd Edition, 2001); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); Maniatis et al., *Molecular Cloning: A Laboratory Manual*

(1982); Ausubel et al., *Current Protocols in Molecular Biology* (John Wiley and Sons, updated July 2008); *Short Protocols in Molecular Biology: A Compendium of Methods from Current Protocols in Molecular Biology*, Greene Pub. Associates and Wiley-Interscience; Glover, *DNA Cloning: A Practical Approach*, vol. I & II (IRL Press, Oxford, 1985); Anand, *Techniques for the Analysis of Complex Genomes*, (Academic Press, New York, 1992); *Transcription and Translation* (B. Hames & S. Higgins, Eds., 1984); Perbal, *A Practical Guide to Molecular Cloning* (1984); and Harlow and Lane, *Antibodies*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1998).

All publications, patents and patent applications cited herein are hereby incorporated by reference in their entirety.

B. Definitions

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by those of ordinary skill in the art to which the invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, preferred embodiments of methods and materials are described herein. For the purposes of the present invention, the following terms are defined below.

The articles “a,” “an,” and “the” are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, “an element” means one element or more than one element.

As used herein, the term “about” or “approximately” refers to a quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length that varies by as much as 30, 25, 20, 15, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1% to a reference quantity, level, value, number, frequency, percentage, dimension, size, amount, weight or length. In particular embodiments, the terms “about” or “approximately” when preceding a numerical value indicates the value plus or minus a range of 15%, 10%, 5%, or 1%.

As used herein, the term “substantially” refers to a quantity, level, concentration, value, number, frequency, percentage, dimension, size, amount, weight or length that is 95%, 96%, 97%, 98%, 99% or 100% of a reference value. For example, a composition that is substantially free of a substance, e.g., a detergent, is 95%, 96%, 97%, 98%, 99% or 100% free of the specified substance, or the substance is undetectable as measured by conventional means. Similar meaning can be applied to the term “absence of,” where referring to the absence of a particular substance or component of a composition.

As used herein, the term “stem cell” refers to a cell which is an undifferentiated cell capable of (1) long term self-renewal, or the ability to generate at least one identical copy of the original cell, (2) differentiation at the single cell level into multiple, and in some instance only one, specialized cell type and (3) of in vivo functional regeneration of tissues. Stem cells are subclassified according to their developmental potential as totipotent, pluripotent, multipotent and oligo/unipotent.

As used herein, the term “adult stem cell” refers to a stem cell found in a developed organism. Adult stem cells include, but are not limited to, ectodermal stem cells, endodermal stem cells, mesodermal stem cells, neural stem cells, hematopoietic stem cells, muscle stem cells, and the like. A muscle stem cell is an example of stem cell that is traditionally thought to be unipotent, giving rise to muscle cells only.

As used herein, the term “satellite stem cell” refers to a type of adult stem cell that gives rise to cells of the myogenic lineage, e.g., myoblasts and myocytes.

As used herein, the term “progenitor cell” refers to a cell that has the capacity to self-renew and to differentiate into more mature cells, but is committed to a lineage (e.g., hematopoietic progenitors are committed to the blood lineage), whereas stem cells are not necessarily so limited. A myoblast is an example of a progenitor cell, which is capable of differentiation to only one type of cell, but is itself not fully mature or fully differentiated. A myoblast may differentiate into a myocyte.

As used herein, the term “myocyte” or “myofiber” refers to a differentiated type of cell found in muscles. Each myocyte contains myofibrils, which are long chains of sarcomeres, the contractile units of the muscle cell. There are various specialized forms of myocytes: cardiac, skeletal, and smooth muscle cells, with various properties known in the art.

As used herein, the term “self-renewal” refers to a cell with a unique capacity to produce unaltered daughter cells and to generate specialized cell types (potency). Self-renewal can be achieved in two ways. Asymmetric cell division produces one daughter cell that is identical to the parental cell and one daughter cell that is different from the parental cell and is a progenitor or differentiated cell. Asymmetric cell division thus does not increase the number of daughter cells identical to the parental cell, but maintains the number of cells of the parental cell type. Symmetric cell division, in contrast, produces two daughter cells that are each identical to the parental cell. Symmetric cell division thus increases the number of cells identical to the parental cell, expanding the population of parental cells. In particular embodiments, symmetric cell division is used interchangeably with “cell expansion.”

As used herein, the term “differentiation” refers to a developmental process whereby cells become specialized for a particular function, for example, where cells acquire one or more morphological characteristics and/or functions different from that of the initial cell type. The term “differentiation” includes both lineage commitment and terminal differentiation processes. States of undifferentiation or differentiation may be assessed, for example, by assessing or monitoring the presence or absence of biomarkers using immunohistochemistry or other procedures known to a person skilled in the art.

As used herein, the term “lineage commitment” refers to the process by which a stem cell becomes committed to forming a particular limited range of differentiated cell types. Lineage commitment arises, for example, when a stem cell gives rise to a progenitor cell during asymmetric cell division. Committed progenitor cells are often capable of self-renewal or cell division.

As used herein, the term “terminal differentiation” refers to the final differentiation of a cell into a mature, fully differentiated cell. Usually, terminal differentiation is associated with withdrawal from the cell cycle and cessation of proliferation.

As used herein, the term “muscle hypertrophy” refers to an increase in muscle size, and may include an increase in individual fiber volume and/or an increase in the cross-sectional area of myofibers, and may also include an increase in the number of nuclei per muscle fiber. Muscle hypertrophy may also include an increase in the volume and mass of whole muscles; however, muscle hypertrophy can be differentiated from muscle hyperplasia, which is an increased number of muscle fibers. In one embodiment, muscular hypertrophy refers to an increase in the number of actin and myosin contractile proteins.

As used herein, the terms “promoting,” “enhancing,” “stimulating,” or “increasing” generally refer to the ability of

a Wnt composition of the invention to produce or cause a greater physiological response (i.e., measurable downstream effect), as compared to the response caused by either vehicle or a control molecule/composition. One such measurable physiological response includes, without limitation, an increase in symmetrical stem cell division compared to asymmetrical cell division, e.g., increase in satellite stem cells, and/or an increase muscle hypertrophy compared to normal, untreated, or control-treated muscle cells. For example, the physiological response may be increased by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 175%, 200%, or greater. In another non-limiting example, muscle hypertrophy in response to administration of a Wnt composition of the invention may be increased by at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 175%, 200%, or greater, compared to normal, untreated, or control-treated muscle. An “increased” or “enhanced” response is typically a “statistically significant” response, and may include an increase that is 1.1, 1.2, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30 or more times (e.g., 500, 1000 times) (including all integers and decimal points in between and above 1, e.g., 1.5, 1.6, 1.7, 1.8, etc.) the response produced by vehicle (the absence of an agent) or a control composition.

As used herein, the terms “retaining” or “maintaining,” or “retain” or “maintain”, generally refer to the ability of a Wnt composition of the invention (i.e., a composition of a modified Wnt) to produce or cause a physiological response (i.e., measurable downstream effect) that is of a similar nature to the response caused by a Wnt composition of the naturally occurring Wnt amino acid or nucleic acid sequence. For example, the Wnt compositions of the invention exhibit Wnt biological activity, and thus retain Wnt activity. The compositions of the invention also produce a physiological response, such as muscle hypertrophy, that is of a similar nature to the response caused by a naturally occurring Wnt polypeptide. A Wnt composition of the invention that elicits a similar physiological response may elicit a physiological response that is at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% or about 100% of the level of physiological response elicited by a composition comprising a naturally occurring Wnt amino acid or nucleic acid sequence.

A modified or engineered Wnt7a polypeptide of the invention that retains the “naturally occurring Wnt7a activity” refers to a modified Wnt7a polypeptide having one or more amino acid mutations, additions, deletions, and/or substitutions that reduce lipidation of the protein, wherein the polypeptide generates a physiological response that is at least 100%, at least 90%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40%, at least 30%, at least 20%, at least 10%, or at least 5% of the physiological response generated by the corresponding naturally occurring Wnt7a polypeptide.

A modified or engineered Wnt5a polypeptide of the invention that retains the “naturally occurring Wnt5a activity” refers to a modified Wnt5a polypeptide having one or more amino acid mutations, additions, deletions, and/or substitutions that reduce lipidation of the protein, wherein the polypeptide generates a physiological response that is at least 100%, at least 90%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40%, at least 30%, at least 20%, at least 10%, or at least 5% of the physiological response generated by the corresponding naturally occurring Wnt5a polypeptide.

As used herein, the terms “decrease” or “lower,” or “lessen,” or “reduce,” or “abate” refers generally to the ability of a Wnt composition of the invention to produce or cause a

lesser physiological response (i.e., downstream effects), as compared to the response caused by either vehicle or a control molecule/composition, e.g., decreased apoptosis. In one embodiment, the decrease can be a decrease in gene expression or a decrease in cell signaling that normally is associated with a reduction of cell viability. A “decrease” or “reduced” response is typically a “statistically significant” response, and may include an decrease that is 1.1, 1.2, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30 or more times (e.g., 500, 1000 times) (including all integers and decimal points in between and above 1, e.g., 1.5, 1.6, 1.7, 1.8, etc.) the response produced by vehicle (the absence of an agent) or a control composition.

C. Wnt Signaling Pathways

The Wnt signaling pathway is an ancient and evolutionarily conserved pathway that regulates crucial aspects of cell fate determination, cell migration, cell polarity, neural patterning and organogenesis during development and throughout adult life. Wnt signaling pathways downstream of the Fz receptor have been identified, including canonical or Wnt/ β -catenin dependent pathways and non-canonical or β -catenin-independent pathways, which can be further divided into Planar Cell Polarity, Wnt/ Ca^{2+} pathways, and others.

Wnt proteins bind to the N-terminal extra-cellular cysteine-rich domain of the Frizzled (Fz) receptor family of which there is ten Fz in humans. The Fz protein is a seven-transmembrane-span protein with topological homology to G-protein coupled receptors. In addition, to the interaction between Wnt and Fz, co-receptors are also required for mediating Wnt signaling. For example the low-density-lipoprotein-related protein5/6 (LRP5/6) is required to mediate the canonical Wnt signal whereas receptor tyrosine kinase RYK may be required for non-canonical functions. Another level of regulation of Wnt signaling occurs in the extra-cellular milieu with the presence of a diverse number of secreted Wnt antagonists. After Wnt binds to a receptor complex, the signal is transduced to cytoplasmic phosphoprotein Dishevelled (Dsh/ Dvl). Dsh can directly interact with Fz. At the level of Dsh, the Wnt signal branches into at least three major cascades, canonical (β -catenin), Planar Cell Polarity and Wnt/ Ca^{2+} . Further, G protein coupled receptor signaling may also stimulate growth and survival pathways such as PI3K.

1. The Canonical Wnt Signaling Pathway

The canonical Wnt signaling pathway was first identified and delineated from genetic screens in *Drosophila* and intensive studies in the fly, worm, frog, fish and mouse have led to the identification of a basic molecular signaling framework. The hallmark of the canonical Wnt pathway is the accumulation and translocation of the adherens junction associated-protein β -catenin into the nucleus. In the absence of Wnt signaling, cytoplasmic β -catenin is degraded by a β -catenin destruction complex, which includes Axin, adenomatous polyposis coli (APC), protein phosphatase 2A (PP2A), glycogen synthase kinase 3 β (GSK3 β) and casein kinase 1 α (CK1 α). Phosphorylation of β -catenin within this complex by CK1 α and GSK3 β targets it for ubiquitination and subsequent proteolytic destruction by the proteasomal machinery. Binding of Wnt to its receptor complex composed of the Fz and the LRP5/6 induces the dual phosphorylation of LRP6 by CK1 and GSK3- β and this allows for the translocation of a protein complex containing Axin from the cytosol to the plasma membrane. Dsh is also recruited to the membrane and binds to Fz and Axin binds to phosphorylated LRP5/6. This complex formed at the membrane at Fz/LRP5/6 induces the stabilization of β -cat via either sequestration and/or degradation of Axin. β -catenin translocates into the nucleus where it

complexes with Lef/Tcf family members to mediate transcriptional induction of target genes.

Canonical Wnt signaling affects formation of anterior head structure and neuroectodermal patterning, posterior patterning and tail formation, as well as for formation of various organ systems including the heart, lungs, kidney, skin and bone.

Wnts that can signal through the canonical Wnt signaling pathway include, but are not limited to, Wnt1, Wnt2, Wnt2b/13, Wnt3, Wnt3a, Wnt8, Wnt8a, Wnt8b, Wnt10a, Wnt10b, and Wnt16.

2. The Non-Canonical Wnt Signaling Pathway

The non-canonical pathway is often referred to as the β -catenin-independent pathway. This pathway can be further divided into at least two distinct branches, the Planar Cell Polarity pathway (or PCP pathway) and the Wnt/ Ca^{2+} pathway, of which only the PCP is discussed in further detail herein. The PCP pathway emerged from genetic studies in *Drosophila* in which mutations in Wnt signaling components including Frizzled and Dishevelled were found to randomize the orientation of epithelial structures including cuticle hairs and sensory bristles. Cells in the epithelia are known to possess a defined apical-basolateral polarity but, in addition, they are also polarized along the plane of the epithelial layer. This rigid organization governs the orientation of structures including orientation of hair follicles, sensory bristles and hexagonal array of the ommatidia in the eye. In vertebrates, this organization has been shown to underlie the organization and orientation of muscle cells, stereo-cilia in the sensory epithelium of the inner ear, the organization of hair follicles, and the morphology and migratory behavior of dorsal mesodermal cells undergoing gastrulation.

Wnt signaling is transduced through Fz independent of LRP5/6 leading to the activation of Dsh. Dsh through Daam1 mediates activation of Rho which in turn activates Rho kinase (ROCK). Daam1 also mediates actin polymerization through the actin binding protein Profilin. Dsh also mediates activation of Rac, which in turn activates JNK. The signaling from Rock, JNK and Profilin are integrated for cytoskeletal changes for cell polarization and motility during gastrulation.

Wnts that can signal through the non-canonical Wnt signaling pathway include, but are not limited to, Wnt4, Wnt5a, Wnt5b, Wnt6, Wnt7a, Wnt7b, and Wnt11.

3. Wnt Signaling in Muscle Cell Development

Satellite stem cells are adult stem cells that give rise to muscle cells. Satellite cells in adult skeletal muscle are located in small depressions between the sarcolemma of their host myofibers and the basal lamina. Upon damage, such as physical trauma, repeated exercise, or in disease, satellite cells become activated, proliferate and give rise to a population of myogenic precursor cells (myoblasts) expressing the myogenic regulatory factors (MRF) MyoD and Myf5. In the course of the regeneration process, myoblasts undergo multiple rounds of division before committing to terminal differentiation, fusing with the host fibers or generating new myofibers to reconstruct damaged tissue (Charge and Rudnicki, 2004). During skeletal muscle regeneration, the satellite cell population is maintained by a stem cell subpopulation, thus allowing tissue homeostasis and multiple rounds of regeneration during the lifespan of an individual (Kuang et al., 2008). Satellite stem cells (Pax7+/Myf5-) represent about 10% of the adult satellite cell pool, and give rise to daughter satellite myogenic cells (Pax7+/Myf5+) through asymmetric apical-basal cell divisions.

Wnt signaling plays a key role in regulating developmental programs through embryonic development, and in regulating stem cell function in adult tissues (Clevers, 2006). Wnts are necessary for embryonic myogenic induction in the paraxial

mesoderm (Borello et al., 2006; Chen et al., 2005; Tajbakhsh et al., 1998), as well in the control of differentiation during muscle fiber development (Anakwe et al., 2003). Recently, the Wnt planar cell polarity (PCP) pathway has been implicated in regulating the orientation of myocyte growth in the developing myotome (Gros et al., 2009). In the adult, Wnt signaling is thought to be necessary for the myogenic commitment of adult stem cells in muscle tissue following acute damage (Poleskaya et al., 2003; Torrente et al., 2004). Other studies suggest that Wnt/ β -catenin signaling regulates myogenic differentiation through activation and recruitment of reserve myoblasts (Rochat et al., 2004). In addition, the Wnt/ β -catenin signaling in satellite cells within adult muscle appears to control myogenic lineage progression by limiting Notch signaling and thus promoting differentiation (Brack et al., 2008).

Recently, it was determined that the Wnt receptor Fzd7 was markedly upregulated in quiescent satellite stem cells. In addition, further studies revealed that Wnt7a is expressed during muscle regeneration and acts through its receptor Fzd7 and Vangl2, a component of the planar cell polarity (PCP) pathway, to induce symmetric satellite stem cell expansion and dramatically enhance muscle regeneration.

Inhibition of receptor or effector molecules in the PCP pathway, e.g., Fzd7 or Vangl2, is believed to abrogate the effects of Wnt7a on satellite stem cells (Le Grand et al., 2009). It has further been demonstrated that administration of lipidated Wnt7a polypeptide, or a polynucleotide encoding a Wnt7a polypeptide that is subsequently post-translationally modified by lipidation, significantly increased satellite stem cell numbers in vitro and in vivo, and promoted tissue formation in vivo, leading to enhanced repair and regeneration in injured and diseased muscle tissue (Le Grand et al., 2009).

Without wishing to be bound to any particular theory, it is contemplated that the mechanism of action of Wnt7a that leads to enhanced repair and regeneration in injured and diseased muscle tissue has two paths: Wnt7a may stimulate the symmetrical expansion of muscle satellite (stem) cells through a PCP pathway, resulting in a larger pool of cells that can subsequently differentiate into myoblasts; and secondly, Wnt7a signaling via the G protein coupled receptor (Frizzled) may stimulate phosphatidylinositol 3-kinase/Akt (protein kinase B)/mammalian target of rapamycin (PI3K/Akt/mTOR) pathway signaling in myoblasts and myofibers, which has been shown to stimulate hypertrophy (Bodine et al., Nature Cell Biology. 2001; vol. 3; pp. 1014-1017; Glass et al., Nature Cell Biology. 2003; vol. 5; pp. 87-90; Ciciliot and Schiaffino, Current Pharmaceutical Design. 2010; 16(8); pp. 906-914). Wnt7a can signal via the G-protein coupled receptor Frizzled 7 and this Wnt/Frz interaction may contribute to both biological effects.

In various embodiments, the invention contemplates, in part, using Wnt compositions comprising one or more modified Wnts that signal through the non-canonical Wnt signaling pathway to repair and regenerate injured muscle tissue. In particular embodiments, the inventive compositions comprise a modified non-canonical Wnt selected from the group consisting of: Wnt4, Wnt5a, Wnt5b, Wnt6, Wnt7a, Wnt7b, and Wnt11. In preferred embodiments, the inventive compositions comprise a modified Wnt5a or Wnt7a polypeptide. In another preferred embodiment, the inventive compositions comprise a modified Wnt5a or Wnt7a polypeptide lacking one or more lipidation sites.

In certain embodiments, the invention compositions comprise a fusion polypeptide comprising a native, heterologous, or hybrid signal peptide, and a non-canonical Wnt polypeptide, optionally lacking one or more lipidation sites.

Although the importance of the PI3K/Akt/mTOR pathway for muscle cell hypertrophy has been described, the therapeutic challenge to specifically stimulate this pathway in muscle cells poses significant obstacles to enhancing repair and regeneration in injured and diseased muscle tissue. Early studies with potent PI3-kinase activators such as IGF-1 produced hypertrophy in vitro but the possibility exists for "off-target" metabolic effects (i.e., IGF-1 and PI3K are key regulators of housekeeping metabolic, survival and metabolic processes). Thus, the potential for a muscle-specific stimulation of a non-canonical Wnt pathway, e.g., Wnt7a-Fzd7 stimulation of PI3K/Akt/mTOR pathway, would represent an important and unique therapeutic breakthrough.

As described in further detail below, the present invention contemplates, in part, inventive Wnt compositions that provide an unexpected solution to this technological hurdle as well as other obstacles to the therapeutic use of Wnt compositions to enhance repair and regeneration in injured and diseased muscle tissue.

D. Polypeptides

Wnt signaling pathways are key components of cell signaling networks. The human Wnt gene family consists of 19 members, encoding evolutionarily conserved glycoproteins with 22 or 24 Cys residues and several conserved Asn and Ser residues. Exemplary human Wnt proteins include Wnt1, Wnt2, Wnt2b/13, Wnt3, Wnt3a, Wnt4, Wnt5a, Wnt5b, Wnt6, Wnt7a, Wnt7b, Wnt8, Wnt8a, Wnt8b, Wnt9a, Wnt9b, Wnt10a, Wnt10b, Wnt11, and Wnt16.

The Wnts are secreted glycoproteins that are heavily modified prior to transport and release into the extra-cellular milieu. After signal sequence cleavage and translocation into the endoplasmic reticulum (ER), Wnts are transported through the endomembrane system to the cell surface and undergo several modifications. Wnts undergo N-linked glycosylation (Burrus and McMahon 1995; Kadowaki et al., 1996; Komekado et al., 2007; Kurayoshi et al., 2007; Mason et al., 1992; Smolich et al., 1993; Tanaka et al. 2002). Many Wnts also are palmitoylated at the first conserved cysteine, e.g., C93 in Wnt1, C77 in Wnt3a, and C104 in Wnt5a (Galli et al., 2007; Kadowaki et al., 1996; Komekado et al., 2007; Willert et al. 2003). In addition, Wnt3a is modified with palmitoleic acid at a conserved serine, 5209, which is also conserved in Wnt1 (S224) Wnt5a (Takada et al., 2006). Furthermore, these conserved cysteine and serine residues are present in many Wnts, e.g., Wnt1, Wnt3a, Wnt4, Wnt5a, Wnt6, Wnt7a, Wnt9a, Wnt10a, and Wnt 11, among others (Takada et al., 2006; see also FIG. 1).

Wnt acylation is widely accepted to cause the notoriously hydrophobic nature of secreted Wnts (Willert et al., 2003). In addition, post-translational lipidation of mammalian Wnts is believed to be important for function. Mutating a conserved N-terminal cysteine of Wnt1, Wnt3a, or Wnt5a prevented palmitoylation in cell culture. These mutant Wnts were secreted but were shown to have little or no signaling activity (Galli et al., 2007; Komekado et al., 2007; Kurayoshi et al., 2007; Willert et al., 2003), and unpalmitoylated Wnts are believed to be unable to bind Fz receptors (Komekado et al., 2007; Kurayoshi et al. 2007). Mutating the conserved serine in the central portion of Wnt3a prevented palmitoleic acid addition and blocked secretion and thus, activity (Takada et al., 2006). Research on *Drosophila* Wg confirmed the importance of acylation (Franch-Marro et al., 2008a; Nusse 2003; van den Heuvel et al., 1993).

Further, these data are supported by the porcupine (porc) phenotype in *Drosophila*, which shows a strong loss of Wg

signaling (van den Heuvel et al., 1993). Porc is an ER-localized integral membrane O-acyl transferase (Kadowaki et al., 1996) required for Wg palmitoylation (Zhai et al., 2004), and for Wg ER exit (Tanaka et al., 2002). Vertebrate Porc also promotes Wnt lipidation and is required for Wnt signaling and Wnt biological activity (Galli et al., 2007).

These studies establish a model in which palmitoleic acid-modification is required for secretion, and palmitate for Fz binding. Thus, Wnt polypeptides lacking either or both of these lipid modifications would be expected to lack biological activity.

In various embodiments, the invention contemplates, in part, Wnt polypeptides that have been modified or engineered to decrease or remove canonical lipidation sites, but that unexpectedly retain Wnt biological activity. In particular embodiments, the inventive Wnt polypeptides promote cell expansion and muscle hypertrophy, and promote tissue formation, regeneration, maintenance and repair. As used herein, the term "canonical" when used in reference to an amino acid sequence, refers to an amino acid or group of amino acids present in the naturally occurring polypeptide. In some contexts, "canonical" is used interchangeably with "native" when referring to amino acids present in the naturally occurring polypeptide.

In certain embodiments, a Wnt polypeptide has been modified or engineered to lack one or more of the native amino acids for lipidation of the Wnt polypeptide. In certain particular embodiments, a Wnt polypeptide has been modified or engineered to lack all of the native amino acids for lipidation of the Wnt polypeptide. In some embodiments, the Wnt polypeptide is a non-canonical Wnt polypeptide, a Wnt polypeptide that signals through a non-canonical Wnt signaling pathway. In particular embodiments, the non-canonical Wnt is selected from the group consisting of: Wnt4, Wnt5a, Wnt5b, Wnt6, Wnt7a, Wnt7b, and Wnt11. In preferred embodiments, the Wnt polypeptide is a Wnt5a or Wnt7a polypeptide that is modified or engineered as discussed herein to lack canonical or native lipidation sites, but that retains or has increased canonical and/or non-canonical Wnt signaling activity.

As noted above, the invention, in embodiments, provides compositions comprising engineered Wnt polypeptides or polynucleotides encoding such engineered Wnt polypeptides, using techniques known and available in the art. In particular embodiments, the Wnt polypeptides are engineered to remove one or more, or all, lipidation sites.

As used herein, the terms "polypeptide," "peptide," and "protein" are used interchangeably, unless specified to the contrary, and according to conventional meaning, i.e., as a sequence of amino acids linked by peptide bonds or modified peptide bonds. In particular embodiments, the term "polypeptide" includes fusion polypeptides. Polypeptides are not limited to a specific length, e.g., they may comprise a full length protein sequence or a fragment of a full length protein, and may include post-translational modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. Polypeptides of the invention may be prepared using any of a variety of well known recombinant and/or synthetic techniques, illustrative examples of which are further discussed below. However, in particular embodiments, Wnt polypeptides of the invention have been engineered such that they have one or more amino acid substitutions, deletions, insertions, or mutations that remove or eliminate one, two, or more or all lipidation sites on the Wnt polypeptide. In certain embodiments, the Wnt polypeptide is a non-canonical Wnt

polypeptide, i.e., a Wnt polypeptide that signals through a non-canonical Wnt signaling pathway.

In various embodiments, the Wnt polypeptide is selected from the group consisting of: Wnt4, Wnt5a, Wnt5b, Wnt6, Wnt7a, Wnt7b, and Wnt11, wherein the Wnt polypeptide lacks, e.g., by amino acid substitution, deletion, or mutation, one or more or all lipidation sites. In preferred embodiments, the Wnt polypeptide is a Wnt5a or Wnt7a polypeptide that lacks, e.g., by amino acid substitution, deletion, or mutation, one or more or all lipidation sites.

As used herein, the term "non-canonical Wnt polypeptide," refers to a Wnt polypeptide that generally or predominantly signals through non-canonical Wnt signaling pathways. Exemplary non-canonical Wnt polypeptides include, but are not limited to Wnt4, Wnt5a, Wnt5b, Wnt6, Wnt7a, Wnt7b, and Wnt11. In some embodiments, the term "non-canonical Wnt polypeptide," refers to a modified or engineered non-canonical Wnt polypeptide having a sequence that is at least about 70%, more preferably about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or about 100%, identical to a naturally occurring non-canonical Wnt polypeptide sequence. Identity may be assessed over at least about 10, 25, 50, 100, 200, 300, or more contiguous amino acids, or may be assessed over the full length of the sequence. Methods for determining % identity or % homology are known in the art and any suitable method may be employed for this purpose. Illustrative examples of non-canonical Wnt polypeptides are set forth in SEQ ID Nos: 2-13 and 15-23, 29-32, and 39.

As used herein, the term "Wnt7a polypeptide," refers to a Wnt7a protein having a polypeptide sequence corresponding to a wild type Wnt7a sequence. In some embodiments, the term "Wnt7a polypeptide," refers to a modified or engineered Wnt7a polypeptide having a sequence that is at least about 70%, more preferably about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or about 100%, identical to a naturally occurring Wnt7a sequence. Identity may be assessed over at least about 10, 25, 50, 100, 200, 300, or more contiguous amino acids, or may be assessed over the full length of the sequence. Illustrative examples of Wnt7a polypeptides are set forth in SEQ ID Nos: 2-13.

As used herein, the term "Wnt5a polypeptide," refers to a Wnt5a protein having a polypeptide sequence corresponding to a wild type Wnt5a sequence. In some embodiments, the term "Wnt5a polypeptide," refers to a modified or engineered Wnt5a polypeptide having a sequence that is at least about 70%, more preferably about 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or about 100%, identical to a naturally occurring Wnt5a sequence. Identity may be assessed over at least about 10, 25, 50, 100, 200, 300, or more contiguous amino acids, or may be assessed over the full length of the sequence. Illustrative examples of Wnt5a polypeptides are set forth in SEQ ID Nos: 15-23.

As used herein, the terms "modified Wnt polypeptide," "modified or engineered Wnt polypeptide," and "engineered Wnt polypeptide," are used interchangeably and refer to a Wnt polypeptide, biologically active fragments or variants thereof, or homolog, paralog, or ortholog thereof that comprises one or more amino acid mutations, additions, deletions, or substitutions. In particular embodiments of the invention, modified Wnt polypeptides comprise one or more amino acid mutations, additions, deletions, and/or substitutions of conserved lipidation sites in order to prevent lipidation of the Wnt polypeptide but that also result in a Wnt polypeptide that retains Wnt biological activity. In particular embodiments, the modified Wnt polypeptide lacks one or more or all lipidation sites but retains Wnt activity. Preferably, modified Wnt

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polypeptides of the invention retain at least 100%, at least 90%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40%, at least 30%, at least 20%, at least 10%, or at least 5% of the naturally occurring Wnt activity.

As used herein, the terms “modified non-canonical Wnt polypeptide,” “modified or engineered non-canonical Wnt polypeptide,” and “engineered non-canonical Wnt polypeptide,” are used interchangeably and refer to a non-canonical Wnt polypeptide, biologically active fragments or variants thereof, or homolog, paralog, or ortholog thereof that comprises one or more amino acid mutations, additions, deletions, or substitutions. In particular embodiments of the invention, modified non-canonical Wnt polypeptides comprise one or more amino acid mutations, additions, deletions, and/or substitutions of conserved lipidation sites in order to prevent lipidation of the non-canonical Wnt polypeptide but that also result in a non-canonical Wnt polypeptide that retains non-canonical Wnt biological activity, e.g., signaling through the non-canonical Wnt pathway. In particular embodiments, the modified non-canonical Wnt polypeptide lacks one or more or all lipidation sites but retains non-canonical Wnt activity. Preferably, modified non-canonical Wnt polypeptides of the invention retain at least 100%, at least 90%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40%, at least 30%, at least 20%, at least 10%, or at least 5% of the naturally occurring non-canonical Wnt activity.

As used herein, the terms “modified Wnt7a polypeptide,” “modified or engineered Wnt7a polypeptide,” and “engineered Wnt7a polypeptide,” are used interchangeably and refer to a Wnt7a polypeptide, biologically active fragments or variants thereof, or homolog, paralog, or ortholog thereof that comprises one or more amino acid mutations, additions, deletions, or substitutions. In particular embodiments, modified Wnt7a polypeptides of the invention comprise one or more amino acid mutations, additions, deletions, and/or substitutions of conserved lipidation sites in order to prevent lipidation of the Wnt7a polypeptide but that also result in a Wnt7a polypeptide that retains or has increased Wnt7a biological activity. In particular embodiments, the modified Wnt7a polypeptide lacks one or more or all lipidation sites but retains Wnt biological activity. Preferably, Wnt7a polypeptide variants of the invention retain at least 100%, at least 90%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40%, at least 30%, at least 20%, at least 10%, or at least 5% of the naturally occurring Wnt7a activity. Illustrative examples of modified Wnt7a polypeptides are set forth in SEQ ID Nos: 3-5 and 12-13.

As used herein, the terms “modified Wnt5a polypeptide,” “modified or engineered Wnt5a polypeptide,” and “engineered Wnt5a polypeptide,” are used interchangeably and refer to a Wnt5a polypeptide, biologically active fragments or variants thereof, or homolog, paralog, or ortholog thereof that comprises one or more amino acid mutations, additions, deletions, or substitutions. In particular embodiments, modified Wnt5a polypeptides of the invention comprise one or more amino acid mutations, additions, deletions, and/or substitutions of conserved lipidation sites in order to prevent lipidation of the Wnt5a polypeptide but that also result in a Wnt5a polypeptide that retains or has increased Wnt5a biological activity. In particular embodiments, the modified Wnt5a polypeptide lacks one or more or all lipidation sites but retains Wnt biological activity. Preferably, Wnt5a polypeptide variants of the invention retain at least 100%, at least 90%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40%, at least 30%, at least 20%, at least 10%, or at least 5% of the

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naturally occurring Wnt5a activity. Illustrative examples of modified Wnt5a polypeptides are set forth in SEQ ID Nos: 16-18.

In particular embodiments, the modified Wnt polypeptides of the invention comprise amino acid mutations, additions, deletions, and/or substitutions that decrease or prevent lipidation of the polypeptide, yet such polypeptides have Wnt biological activity. In particular embodiments, the Wnt polypeptide is a canonical Wnt polypeptide comprising an amino acid mutation, addition, deletion, and/or substitution at one or more of the amino acid positions identified in Table 1, wherein the amino acid mutation, addition, deletion, and/or substitution prevents lipidation at the identified position, and wherein the canonical Wnt polypeptide retains or has increased levels of canonical Wnt biological activity.

TABLE 1

Wnt	AA positions	Ref. SEQ ID
Wnt1	93; 224	24
Wnt2	76; 212	25
Wnt2b	88; 224	26
Wnt3	80; 212	27
Wnt3a	77; 209	28
Wnt8a	54; 186	33
Wnt8b	54; 186	34
Wnt9a	93; 221	35
Wnt9b	89; 216	36
Wnt10a	96; 268	37
Wnt10b	83; 253	38
Wnt16	81; 227	40

In particular embodiments, the Wnt polypeptide is a non-canonical Wnt polypeptide comprising an amino acid mutation, addition, deletion, and/or substitution at one or more of the amino acid positions identified in Table 2, wherein the amino acid mutation, addition, deletion, and/or substitution prevents lipidation at the identified position, and wherein the non-canonical Wnt polypeptide retains or has increased levels of non-canonical Wnt biological activity.

TABLE 2

Wnt	AA positions	Ref. SEQ ID
Wnt4	78; 212	29
Wnt5a	104; 244	15
Wnt5b	83; 223	30
Wnt6	76; 228	31
Wnt7a	73; 206	2
Wnt7b	73; 206	32
Wnt11	80; 215	39

In particular embodiments, the Wnt polypeptide is a Wnt7a polypeptide comprising an amino acid mutation, addition, deletion, and/or substitution at amino acid 73 and/or 206 that prevents lipidation at such position(s), wherein the Wnt7a polypeptide retains or has increased levels of Wnt7a biological activity. In one embodiment, the polypeptide is a Wnt7a polypeptide comprising an amino acid mutation, addition, deletion, and/or substitution at amino acid position 73 that prevents lipidation at this position, wherein the Wnt7a polypeptide retains or has increased levels of Wnt7a biological activity. In some embodiments, the Wnt polypeptide of the invention is a Wnt7a polypeptide comprising an amino acid mutation, addition, deletion, and/or substitution at amino acid position 206 that prevents lipidation of Wnt7a at this position, wherein the Wnt7a polypeptide retains or has increased levels of Wnt7a biological activity. In some embodiments, the polypeptide is a Wnt7a polypeptide comprising amino acid

mutations, additions, deletions, and/or substitutions at amino acid positions 73 and 206, wherein the Wnt7a polypeptide lacks post-translational lipidation and has Wnt biological activity.

In certain embodiments, the C73 and/or S206 of a Wnt7a polypeptide are substituted with Ala or another amino acid that prevents lipidation of these residues. In other embodiments, C73 and/or S206 are mutated or deleted to prevent lipidation of these residues, e.g., SEQ ID Nos: 3-5. In some embodiments, C73 and S206 are substituted with Ala, and the Wnt7a polypeptide of the invention lacks lipidation sites and retains some level of Wnt biological activity e.g., SEQ ID NO: 5.

In particular embodiments, the Wnt polypeptide is a Wnt5a polypeptide comprising an amino acid mutation, addition, deletion, and/or substitution at amino acid 104 and/or 244 that prevents lipidation at such position(s), wherein the Wnt5a polypeptide retains or has or increased levels of Wnt5a biological activity. In one embodiment, the polypeptide is a Wnt5a polypeptide comprising an amino acid mutation, addition, deletion, and/or substitution at amino acid position 104 that prevents lipidation at this position, wherein the Wnt5a polypeptide retains or has increased levels of Wnt5a biological activity. In some embodiments, the Wnt polypeptide of the invention is a Wnt5a polypeptide comprising an amino acid mutation, addition, deletion, and/or substitution at amino acid position 244 that prevents lipidation of Wnt5a at this position, wherein the Wnt5a polypeptide retains or has increased levels of Wnt5a biological activity. In some embodiments, the polypeptide is a Wnt5a polypeptide comprising amino acid mutations, additions, deletions, and/or substitutions at amino acid positions 104 and 244, wherein the Wnt5a polypeptide lacks post-translational lipidation and has Wnt biological activity.

In certain embodiments, the C104 and/or S244 of a Wnt5a polypeptide are substituted with Ala or another amino acid that prevents lipidation of these residues. In other embodiments, C104 and/or S244 are mutated or deleted to prevent lipidation of these residues, e.g., SEQ ID Nos: 16-18. In some embodiments, C104 and S244 are substituted with Ala, and the Wnt5a polypeptide of the invention lacks lipidation sites and retains some level of Wnt biological activity e.g., SEQ ID NO: 18.

As used herein, the term “naturally occurring”, refers to a polypeptide or polynucleotide sequence that can be found in nature. For example, a naturally occurring polypeptide or polynucleotide sequence would be one that is present in an organism, and can be isolated from the organism, and which has not been intentionally modified by man in the laboratory. The term “wild-type” is often used interchangeably with the term “naturally occurring.”

In the context of the invention, a polypeptide, a biologically active fragment or variant thereof, or homolog, paralog, or ortholog thereof, is considered to have at least substantially the same activity as the wild-type protein when it exhibits about 10%, 20%, 30%, 40% or 50% of the activity of the wild-type protein, preferably at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, or at least 80% of the activity of the wild type protein. In particular embodiments, the polypeptide, a biologically active fragment or variant thereof, or homolog, paralog, or ortholog thereof, exhibits at least 70%, at least 80%, at least 90%, at least 95% or about 100% of the activity of the wild-type protein. In certain embodiments, an activity greater than wild type activity may be achieved. Activity of a non-canonical Wnt polypeptide, e.g., a Wnt 5a or Wnt7a polypeptide, a biologically active fragment or variant thereof, or homolog, paralog,

or ortholog thereof, for example, can be determined by measuring its ability to mimic wild-type Wnt biological activity by, for example, stimulating the Wnt signaling pathway, such as by promoting symmetrical stem cell expansion or cell growth, and comparing the ability to the activity of a wild type protein. Methods of measuring and characterizing stem cell division, e.g., satellite stem cell division, and cell growth, e.g., muscle hypertrophy are known in the art.

As used herein, the term “biologically active fragment,” as applied to fragments of a reference polynucleotide or polypeptide sequence, refers to a fragment of a modified Wnt polypeptide that has at least about 5, 10, 15, 20, 25, 30, 40, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99, 100, 110, 120, 150, 200, 300, 400, 500, 600, 700, 800, 900, or 1000% or more of the biological activity of a Wnt reference sequence, such as its biological activity to stimulate the Wnt signaling pathway. Certain embodiments of the present invention contemplate, in part, biologically active fragments of a modified Wnt polypeptide of at least about 20, 50, 100, 150, 200, 250, or 300 contiguous amino acid residues in length or polynucleotide sequences encoding the same, including all integers in between, which comprise or encode a polypeptide having the biological activity of a reference Wnt polypeptide, e.g., a naturally occurring Wnt polypeptide.

Modified polypeptides include polypeptide variants. The term “variant” as used herein, refers to polypeptides that are distinguished from a reference polypeptide by the modification, addition, deletion, or substitution of at least one amino acid residue, as discussed elsewhere herein and as understood in the art. In certain embodiments, a polypeptide variant is distinguished from a reference polypeptide by one or more amino acid substitutions (e.g., 1, 2, 3, 4, 5 or more substitutions), which may be conservative or non-conservative. For example, in various embodiments, one or more conservative or non-conservative substitutions can be made in any amino acid residue that is targeted for lipidation in the naturally occurring Wnt polypeptide.

In other particular embodiments, Wnt polypeptide variants comprise one or more amino acid additions, deletions, or substitutions in order to prevent lipidation, to increase Wnt pathway signaling activity, and/or to increase stability of the modified Wnt polypeptide compared to the naturally occurring Wnt polypeptide.

In other particular embodiments, non-canonical Wnt polypeptide variants comprise one or more amino acid additions, deletions, or substitutions in order to prevent lipidation, to increase Wnt pathway signaling activity, and/or to increase stability of the modified Wnt polypeptide compared to the naturally occurring non-canonical polypeptide.

In other particular embodiments, Wnt7a polypeptide variants comprise one or more amino acid additions, deletions, or substitutions in order to prevent lipidation, to increase Wnt pathway signaling activity, and/or to increase stability of the modified Wnt polypeptide compared to the naturally occurring Wnt7a polypeptide.

In other particular embodiments, Wnt5a polypeptide variants comprise one or more amino acid additions, deletions, or substitutions in order to prevent lipidation, to increase Wnt pathway signaling activity, and/or to increase stability of the modified Wnt polypeptide compared to the naturally occurring Wnt5a polypeptide.

To generate such variants, one skilled in the art, for example, can change one or more of the codons of the encoding DNA sequence, e.g., according to Table 3.

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TABLE 3

Amino Acid Codons					
Amino Acids	Codons				
Alanine	GCA	GCC	GCG	GCU	
Cysteine	UGC	UGU			
Aspartic acid	GAC	GAU			
Glutamic acid	GAA	GAG			
Phenylalanine	UUC	UUU			
Glycine	GGA	GGC	GGG	GGU	
Histidine	CAC	CAU			
Isoleucine	AUA	AUC	AUU		
Lysine	AAA	AAG			
Leucine	UUA	UUG	CUA	CUC	CUG CUU
Methionine	AUG				
Asparagine	AAC	AAU			
Proline	CCA	CCC	CCG	CCU	
Glutamine	CAA	CAG			
Arginine	AGA	AGG	CGA	CGC	CGG CGU
Serine	AGC	AGU	UCA	UCC	UCG UCU
Threonine	ACA	ACC	ACG	ACU	
Valine	GUA	GUC	GUG	GUU	
Tryptophan	UGG				
Tyrosine	UAC	UAU			

Guidance in determining which amino acid residues can be substituted, inserted, or deleted without abolishing biological or immunological activity can be found using computer programs well known in the art, such as DNASTAR™ software. If desired, amino acid substitutions can be made to change and/or remove functional groups from a polypeptide. Alternatively, amino acid changes in the protein variants disclosed herein can be conservative amino acid changes, i.e., substitutions of similarly charged or uncharged amino acids. A conservative amino acid change involves substitution of one of a family of amino acids which are related in their side chains. Naturally occurring amino acids are generally divided into four families: acidic (aspartate, glutamate), basic (lysine, arginine, histidine), non-polar (alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), and uncharged polar (glycine, asparagine, glutamine, cystine, serine, threonine, tyrosine) amino acids. Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. See TABLE 4.

TABLE 4

Conservative Amino Acid Substitutions	
Original residue	Conservative substitution
Ala (A)	Gly; Ser
Arg (R)	Lys
Asn (N)	Gln; His
CI (C)	Ser
Gln (Q)	Asn
Glu (E)	Asp
Gly (G)	Ala; Pro
His (H)	Asn; Gln
Ile (I)	Leu; Val
Leu (L)	Ile; Val
Lys (K)	Arg; Gln; Glu
Met (M)	Leu; Tyr; Ile
Phe (F)	Met; Leu; Tyr
Ser (S)	Thr
Thr (T)	Ser
Trp (W)	Tyr
Tyr (Y)	Trp; Phe
Val (V)	Ile; Leu

Other substitutions also are permissible and can be determined empirically or in accord with other known conservative (or non-conservative) substitutions.

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In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, i.e., still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity.

Variants of the polypeptides of the invention include glycosylated forms, aggregative conjugates with other molecules, and covalent conjugates with unrelated chemical moieties (e.g., pegylated molecules). Covalent variants can be prepared by linking functionalities to groups which are found in the amino acid chain or at the N- or C-terminal residue, as is known in the art. Variants also include allelic variants, species variants, and muteins. Truncations or deletions of regions which do not affect functional activity of the proteins are also variants.

Amino acids in polypeptides of the present invention that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, *Science* 244: 1081-1085, 1989). Sites that are critical for ligand-receptor binding can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith et al., *J. Mol. Biol.* 224:899-904, 1992 and de Vos et al. *Science* 255:306-312, 1992).

Certain changes do not significantly affect the folding or activity of the protein. The number of amino acid substitutions a skilled artisan would make depends on many factors, including those described above. Generally speaking, the number of substitutions for any given polypeptide will not be more than 50, 40, 30, 25, 20, 15, 10, 5 or 3.

In addition, pegylation of polypeptides and/or muteins is expected to provide improved properties, such as increased half-life, solubility, and protease resistance. Pegylation is well known in the art.

E. Fusion Polypeptides

In various embodiments, the present invention contemplates, in part, fusion polypeptides, and polynucleotides encoding fusion polypeptides. In one embodiment, the fusion polypeptide comprises a modified Wnt polypeptide, a biologically active Wnt polypeptide fragment, and/or such peptides further comprising one or more amino acid mutations, substitutions, and/or additions, as described elsewhere herein. In a particular embodiment, the fusion polypeptide comprises a non-canonical Wnt polypeptide selected from the group consisting of: Wnt4, Wnt5a, Wnt5b, Wnt6, Wnt7a, Wnt7b, and Wnt11. In preferred embodiments, the Wnt polypeptide is a Wnt5a or Wnt7a polypeptide that is modified or engineered as discussed herein to lack canonical or native lipidation sites, but that retains or has increased Wnt signaling activity.

Fusion polypeptides may comprise a signal peptide at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the Wnt polypeptides. Fusion polypeptides may also comprise linkers or spacers,

one or more protease cleavage sites, one or more epitope tags or other sequence for ease of synthesis, purification or production of the polypeptide.

Fusion polypeptide and fusion proteins refer to a polypeptide of the invention that has been covalently linked, either directly or via an amino acid linker, to one or more heterologous polypeptide sequences (fusion partners). The polypeptides forming the fusion protein are typically linked C-terminus to N-terminus, although they can also be linked C-terminus to C-terminus, N-terminus to N-terminus, or N-terminus to C-terminus. The polypeptides of the fusion protein can be in any order.

The fusion partner may be designed and included for essentially any desired purpose provided they do not adversely affect the desired activity of the polypeptide. For example, in one embodiment, fusion partners may be selected so as to increase the solubility or stability of the protein, to facilitate production and/or purification of a Wnt polypeptide, and/or to facilitate systemic delivery and/or tissue uptake of Wnts. Fusion polypeptides may be produced by chemical synthetic methods or by chemical linkage between the two moieties or may generally be prepared using other standard techniques. In one embodiment, a Wnt fusion polypeptide comprises one or more of, or all of: a signal peptide, a Wnt polypeptide, e.g., a non-canonical Wnt such as Wnt5a or Wnt7a, or a biologically active fragment thereof, a protease cleavage site, and an epitope tag.

As used herein, the term "signal peptide" refers to a leader sequence ensuring entry into the secretory pathway. For industrial production of a secreted protein, the protein to be produced needs to be secreted efficiently from the host cell or the host organism. The signal peptide may be, e.g., the native signal peptide of the protein to be produced, a heterologous signal peptide, or a hybrid of native and heterologous signal peptide. Numerous signal peptides are used for production of secreted proteins.

Thus, in various embodiment, the present invention contemplates a method of improving the production and secretion of Wnt polypeptides, including non-canonical Wnt polypeptides such as Wnt4, Wnt5a, Wnt5b, Wnt6, Wnt7a, Wnt7b, and Wnt11, comprising expressing in cells, e.g., mammalian, insect, or bacterial, a fusion polypeptide having a signal peptide and a non-canonical Wnt polypeptide that has been modified or engineered as discussed herein to lack canonical or native lipidation sites, wherein the polypeptide retains or has increased canonical and/or non-canonical Wnt signaling activity. In preferred embodiments, a method of improving the production and secretion of Wnt5a or Wnt7a comprises expressing in cells a fusion polypeptide having a signal peptide and a Wnt5a or Wnt7a polypeptide that has been modified or engineered as discussed herein to lack canonical or native lipidation sites, but that retains or has increased canonical and/or non-canonical Wnt signaling activity.

Illustrative examples of signal peptides for use in fusion polypeptides of the invention include, but are not limited to: a CD33 signal peptide; an immunoglobulin signal peptide, e.g., an IgGκ signal peptide or an IgGμ signal peptide; a growth hormone signal peptide; an erythropoietin signal peptide; an albumin signal peptide; a secreted alkaline phosphatase signal peptide, and a viral signal peptide, e.g., rotavirus VP7 glycoprotein signal peptide.

In particular embodiments, the inventive fusion polypeptides comprise protease cleavage sites and epitope tags to facilitate purification and production of non-canonical Wnt polypeptides, e.g., Wnt5a and Wnt7a. The position of the protease cleavage site is typically between the C-terminus of

the Wnt polypeptide and the epitope tag to facilitate removal of heterologous sequences prior to delivery of the Wnt to a cell or tissue.

Illustrative examples of heterologous protease cleavage sites that can be used in fusion proteins of the invention include, but are not limited to: a tobacco etch virus (TEV) protease cleavage site, a heparin cleavage site, a thrombin cleavage site, an enterokinase cleavage site and a Factor Xa cleavage site.

Illustrative examples of epitope tags that can be used in fusion proteins of the invention include, but are not limited to: a HIS6 epitope, a MYC epitope, a FLAG epitope, a V5 epitope, a VSV-G epitope, and an HA epitope.

A peptide linker sequence may also be employed to separate the fusion polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures, if desired. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Certain peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46 (1985); Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262 (1986); U.S. Pat. No. 4,935,233 and U.S. Pat. No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference. The two coding sequences can be fused directly without any linker or by using a flexible polylinker composed of the pentamer Gly-Gly-Gly-Gly-Ser repeated 1 to 3 times. Such linker has been used in constructing single chain antibodies (scFv) by being inserted between VH and VL (Bird et al., 1988, *Science* 242:423-426; Huston et al., 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:5979-5883). The linker is designed to enable the correct interaction between two beta-sheets forming the variable region of the single chain antibody. Other linkers which may be used include Glu-Gly-Lys-Ser-Ser-Gly-Ser-Gly-Ser-Glu-Ser-Lys-Val-Asp (Chaudhary et al., 1990, *Proc. Natl. Acad. Sci. U.S.A.* 87:1066-1070) and Lys-Glu-Ser-Gly-Ser-Val-Ser-Ser-Glu-Gln-Leu-Ala-Gln-Phe-Arg-Ser-Leu-Asp (Bird et al., 1988, *Science* 242:423-426).

In one embodiment, fusion polypeptides of the invention comprise a portion of an antibody, such as an immunoglobulin "Fc region", and a modified Wnt polypeptide, such as a Wnt5a or Wnt7a polypeptide, that has been modified or engineered as discussed herein to lack canonical or native lipidation sites, but that retains or has increased canonical and/or non-canonical Wnt signaling activity. The Fc region of the antibody is composed of two heavy chains that contribute two or three constant domains depending on the class of the antibody. The Fc region can be obtained from any of the classes of immunoglobulin, IgG, IgA, IgM, IgD and IgE. In some embodiments, the Fc region is a wild-type Fc region. In some embodiments, the Fc region is a mutated Fc region. In some embodiments, the Fc region is truncated at the N-terminal end by 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids, (e.g., in the hinge

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domain). Wnt fusion polypeptides of the invention comprising an Fc region may have improved production and/or purification efficiencies.

In one embodiment, the Wnt fusion polypeptide of the invention comprises a Wnt7a polypeptide modified to lack native lipidation sites, but that retains non-canonical Wnt signaling activity, and a human IgG Fc region. In a specific embodiment, the Wnt7a polypeptide comprises an amino acid deletion, insertion, or substitution at the amino acid position corresponding to position 73 or 206 of SEQ ID NO: 2, and a human IgG Fc region. In a specific embodiment, the Wnt7a polypeptide comprises amino acid deletions, insertions, or substitutions at the amino acid positions corresponding to positions 73 and 206 of SEQ ID NO: 2, and a human IgG Fc region. In a specific embodiment, the Wnt7a polypeptide comprises alanine at the amino acid position corresponding to position 73 or 206 of SEQ ID NO: 2, and a human IgG Fc region. In one embodiment, the Wnt7a polypeptide comprises alanine at the amino acid positions corresponding to positions 73 and 206 of SEQ ID NO: 2, and a human IgG Fc region.

Fusion polypeptides comprising an Fc region and a modified non-canonical Wnt polypeptide, e.g., Wnt5a or Wnt7a, may further comprise one or more of, or all of a native or heterologous signal peptide, protease cleavage sites and epitope tags.

In preferred embodiments, a method of improving the half-life, pharmacokinetic properties, solubility, and production efficiency of a modified Wnt5a or Wnt7a polypeptide comprises expressing in cells a fusion polypeptide having an Fc region and/or signal peptide and a Wnt5a or Wnt7a polypeptide that has been modified or engineered as discussed herein to lack canonical or native lipidation sites, but that retains or has increased canonical and/or non-canonical Wnt signaling activity.

For example, a modified Wnt5a or Wnt7a polypeptide fused to an immunoglobulin Fc region has increased systemic half-life, improved pharmacokinetic properties, solubility and production efficiency. In one embodiment, fusing a Wnt polypeptide to an Fc portion of an antibody optimizes the pharmacokinetic and pharmacodynamic properties of the fusion polypeptide. For example, the Fc portion of the polypeptide may protect the polypeptide from degradation, keeping the polypeptide in circulation longer. In general, polypeptides, fusion polypeptides (as well as their encoding polynucleotides), and cells are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, an "isolated peptide" or an "isolated polypeptide" and the like, as used herein, refer to in vitro isolation and/or purification of a peptide or polypeptide molecule from a cellular environment, and from association with other components of the cell, i.e., it is not significantly associated with in vivo substances. Similarly, an "isolated polynucleotide," as used herein, refers to a polynucleotide that has been purified from the sequences which flank it in a naturally-occurring state, e.g., a DNA fragment that has been removed from the sequences that are normally adjacent to the fragment. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment. An "isolated cell" refers to a cell that has been obtained from an in vivo tissue or organ and is substantially free of extracellular matrix. Preferably, a polypeptide, polynucleotide, or cell is isolated if it is at least about 60% pure, at least about 70% pure, at least about 80% pure, at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure.

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As used herein, the term "obtained from" means that a sample such as, for example, a polynucleotide or polypeptide is isolated from, or derived from, a particular source, such as a recombinant host cell. In another embodiment, the term "obtained from" refers to a cell isolated from or derived from a source such as an in vivo tissue or organ.

F. Polynucleotides

The present invention also provides isolated polynucleotides that encode Wnt polypeptides of the invention. In various embodiments, the present invention contemplates, in part, Wnt polynucleotides that encode polypeptides that lack canonical lipidation sites, but that retain Wnt biological activity, and in some embodiments have increased Wnt signaling activity. In particular embodiments, the inventive Wnt polynucleotides encode Wnt polypeptides that promote stem cell expansion and promote tissue formation, regeneration, maintenance and repair.

The inventive Wnt polynucleotides are suitable for clinical scale production of Wnt polypeptides and for use in methods of enhancing repair and regeneration in injured and diseased muscle tissue in humans. In certain embodiments, a Wnt polynucleotide encodes a Wnt polypeptide that lacks one or more of the native amino acids for lipidation of the Wnt polypeptide. In certain particular embodiments, a Wnt polynucleotide encodes a Wnt polypeptide that lacks all of the native amino acids for lipidation of the Wnt polypeptide. In preferred embodiments, the Wnt polynucleotide encodes a non-canonical Wnt polypeptide that lacks canonical lipidation sites, but retains or has increased Wnt biological activity. In other preferred embodiments, the Wnt polynucleotide encodes a Wnt5a or Wnt7a polypeptide that lacks canonical lipidation sites, but retains or has increased Wnt biological activity, such as non-canonical Wnt signaling activity.

Nucleic acids can be synthesized using protocols known in the art as described in Caruthers et al., 1992, *Methods in Enzymology* 211, 3-19; Thompson et al., *International PCT Publication No. WO 99/54459*; Wincott et al., 1995, *Nucleic Acids Res.* 23, 2677-2684; Wincott et al., 1997, *Methods Mol. Bio.*, 74, 59-68; Brennan et al., 1998, *Biotechnol Bioeng.*, 61, 33-45; and Brennan, U.S. Pat. No. 6,001,311).

By "nucleotide" is meant a heterocyclic nitrogenous base in N-glycosidic linkage with a phosphorylated sugar. Nucleotides are recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other (see for example, Usman and McSwiggen, supra; Eckstein et al., *International PCT Publication No. WO 92/07065*; Usman et al., *International PCT Publication No. WO 93/15187*; Uhlman & Peyman, supra). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach et al., (1994, *Nucleic Acids Res.* 22, 2183-2196).

As used herein, the terms "DNA" and "polynucleotide" and "nucleic acid" refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. Therefore, a DNA segment encoding a polypeptide refers to a DNA segment that contains one or more coding sequences yet is substantially isolated away from, or purified free from, total genomic DNA of the species from which the DNA segment is obtained. Included within the terms "DNA segment" and

“polynucleotide” are DNA segments and smaller fragments of such segments, and also recombinant vectors, including, for example, plasmids, cosmids, phagemids, phage, viruses, and the like.

As will be understood by those skilled in the art, the polynucleotide sequences of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides, and the like. Such segments may be naturally isolated, recombinant, or modified synthetically by the hand of man.

As will be recognized by the skilled artisan, polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (i.e., an endogenous sequence that encodes a polypeptide of the invention or a portion thereof) or may comprise a variant, or a biological functional equivalent of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions, as described elsewhere herein, preferably such that the variant encodes a polypeptide that lacks canonical lipidation sites, but retains, and in some embodiments, has increased biological activity, such as pathway signaling activity.

Also included are polynucleotides that hybridize to polynucleotides that encode a polypeptide of the invention. To hybridize under “stringent conditions” describes hybridization protocols in which nucleotide sequences at least 60% identical to each other remain hybridized. High stringency hybridization conditions are conditions that enable a probe, primer or oligonucleotide to hybridize only to its target sequence. Stringent conditions are sequence-dependent and will differ. Moderately stringent conditions are conditions that use washing solutions and hybridization conditions that are less stringent (Sambrook, 1989) than those for high stringency, such that a polynucleotide will hybridize to the entire, fragments, derivatives or analogs of nucleic acids of the present invention. Moderate stringency conditions are described in (Ausubel et al., 1987; Kriegler, 1990). Low stringency conditions are conditions that use washing solutions and hybridization conditions that are less stringent than those for moderate stringency (Sambrook, 1989), such that a polynucleotide will hybridize to the entire, fragments, derivatives or analogs of nucleic acids of the present invention. Conditions of low stringency, such as those for cross-species hybridizations are described in (Ausubel et al., 1987; Kriegler, 1990; Shilo and Weinberg, 1981).

In additional embodiments, the invention provides isolated polynucleotides comprising various lengths of contiguous stretches of sequence identical to or complementary to a polynucleotide encoding a polypeptide as described herein. For example, polynucleotides provided by this invention encode at least about 50, 100, 150, 200, 250, 300, or about 350 or more contiguous amino acid residues of a polypeptide of the invention, as well as all intermediate lengths. It will be readily understood that “intermediate lengths”, in this context, means any length between the quoted values, such as 56, 57, 58, 59, etc., 101, 102, 103, etc.; 151, 152, 153, etc.; 201, 202, 203, etc.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as

described herein, including polynucleotides that are optimized for human and/or primate codon selection. Further, alleles of the genes comprising the polynucleotide sequences provided herein may also be used.

Polynucleotides compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques (see generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, N.Y., 1989, and other like references).

A variety of expression vector/host systems are known and may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems.

As used herein, the terms “control elements” or “regulatory sequences” refer to those sequences present in an expression vector that are non-translated regions of the vector, e.g., enhancers, promoters, 5' and 3' untranslated regions, and interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUE-SCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPT1 plasmid (Gibco BRL, Gaithersburg, Md.), pET plasmid (Novagen) and the like may be used. The vector components generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter that is recognized by the host organism, and a transcription termination sequence. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest.

In the yeast *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. Also included are *Pichia pandoris* expression systems (see, e.g., Li et al., *Nature Biotechnology*, 24, 210-215, 2006; and Hamilton et al., *Science*, 301:1244, 2003).

In cases where plant expression vectors are used, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, *EMBO J.* 6:307-311 (1987)). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection.

An insect system may also be used to express a polypeptide of interest. Exemplary baculovirus expression systems, include, but are not limited to those that utilize SF9, SF21, and Tni cells (see, e.g., Murphy and Piwnicka-Worms, *Curr Protoc Protein Sci.* Chapter 5: Unit 5.4, 2001).

In mammalian host cells, a number of viral-based expression systems are generally available. In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. Examples of useful mammalian host cell lines include COS-7 cells, 293 or 293T cells, BHK cells, VERO-76 cells, HELA cells, and CHO cells, including DHFR-CHO

cells. Mammalian expression systems can utilize attached cell lines, for example, in T-flasks, roller bottles, or cell factories, or suspension cultures, for example, in 1 L and 5 L spinners, 5 L, 14 L, 40 L, 100 L and 200 L stir tank bioreactors, or 20/50 L and 100/200 L WAVE bioreactors, among others known in the art.

Also included is cell-free expression of proteins. These and related embodiments typically utilize purified RNA polymerase, ribosomes, tRNA and ribonucleotides; these reagents may be produced by extraction from cells or from a cell-based expression system.

In particular embodiments, polypeptides of the invention are expressed and purified from bacteria. Exemplary bacterial expression vectors include, BLUESCRIPT (Stratagene); pIN vectors (Van Heeke & Schuster, *J. Biol. Chem.* 264:5503-5509 (1989)); and pGEX Vectors (Promega, Madison, Wis.) which may be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). Certain embodiments may employ *E. coli*-based expression systems.

In specific embodiments, protein expression may be controlled by a T7 RNA polymerase (e.g., pET vector series). These and related embodiments may utilize the expression host strain BL21(DE3), a λ DE3 lysogen of BL21 that supports T7-mediated expression and is deficient in lon and ompT proteases for improved target protein stability. Also included are expression host strains carrying plasmids encoding tRNAs rarely used in *E. coli*, such as Rosetta™ (DE3) and Rosetta 2 (DE3) strains. Cell lysis and sample handling may also be improved using reagents such as Benzonase® nuclease and BugBuster® Protein Extraction Reagent. For cell culture, auto-inducing media can improve the efficiency of many expression system, including high-throughput expression systems. Media of this type (e.g., Overnight Express™ Autoinduction System) gradually elicit protein expression through metabolic shift without the addition of artificial inducing agents such as IPTG. Certain embodiments may employ a cold-shock induced *E. coli* high-yield production system, because over-expression of proteins in *Escherichia coli* at low temperature improves their solubility and stability (see, e.g., Qing et al., *Nature Biotechnology*. 22:877-882, 2004).

The protein produced by a recombinant cell can be purified and characterized according to a variety of techniques. Exemplary systems for performing protein purification and analyzing protein purity include fast protein liquid chromatography (FPLC) (e.g., AKTA and Bio-Rad FPLC systems), high-pressure liquid chromatography (HPLC) (e.g., Beckman and Waters HPLC). Exemplary chemistries for purification include ion exchange chromatography (e.g., Q, S), size exclusion chromatography, salt gradients, affinity purification (e.g., Ni, Co, FLAG, maltose, glutathione, protein A/G), gel filtration, reverse-phase, ceramic HyperD® ion exchange chromatography, and hydrophobic interaction columns (HIC), among others known in the art. Also included are analytical methods such as SDS-PAGE (e.g., coomassie, silver stain), immunoblot, Bradford, and ELISA, which may be utilized during any step of the production or purification process, typically to measure the purity of the protein composition.

In certain embodiments, clinical grade proteins can be isolated from *E. coli* inclusion bodies. In particular embodiments, the present invention contemplates methods for producing a recombinant Wnt polypeptide that is suitable for therapeutic uses, as described elsewhere herein.

In one embodiment, a method for producing a recombinant Wnt polypeptide includes one or more of the following steps: i) expression of a Wnt polynucleotide in a host; ii) culturing

the host cell to express the Wnt polypeptide as inclusion bodies; iii) one or more steps of washing the inclusion bodies; iv) solubilizing the polypeptide; v) refolding the polypeptide; vi) purifying the polypeptide; and vii) dialyzing the polypeptide in a desired buffer.

In certain embodiments, Wnt polynucleotide sequences are codon optimized for expression in a bacterial host.

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield, *J. Am. Chem. Soc.* 85:2149-2154 (1963)). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

G. Compositions

In various embodiments, the invention contemplates, in part, novel compositions of Wnt polypeptides and polynucleotides encoding the same. As discussed elsewhere herein, one of the major limitations or obstacles to the therapeutic use of Wnts is their low solubility, which makes them impracticable to generate on a clinical scale. The inventors have engineered novel Wnt polypeptides that have increased solubility, stability, and that retain or have increased Wnt biological activity compared to naturally occurring Wnts. In particular embodiments, the invention provides aqueous formulations of soluble Wnt polypeptides to promote stem cell expansion and muscle hypertrophy, and promote tissue formation, regeneration, maintenance and repair. In certain embodiments, the invention provides aqueous formulations of soluble Wnt polypeptides to promote stem cell expansion and muscle hypertrophy, and promote tissue formation, regeneration, maintenance and repair, wherein detergents are substantially absent from the formulations.

The compositions of the invention may comprise one or more polypeptides, polynucleotides, vectors comprising same, etc., as described herein, and one or more pharmaceutically-acceptable salts or carriers and/or physiologically-acceptable solutions for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy. It will also be understood that, if desired, the compositions of the invention may be administered in combination with other agents as well, such as, e.g., other proteins, polypeptides, small molecules or various pharmaceutically-active agents. There is virtually no limit to other components that may also be included in the compositions, provided that the additional agents do not adversely affect the therapeutic potential of the Wnt composition, such as the ability of the composition to promote muscle hypertrophy and promote tissue formation, regeneration, maintenance and repair.

Pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and those formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like.

In certain circumstances it will be desirable to deliver the compositions disclosed herein parenterally, intravascularly,

e.g., intravenously or intraarterially, intramuscularly, or even intraperitoneally as described, for example, in U.S. Pat. No. 5,543,158; U.S. Pat. No. 5,641,515 and U.S. Pat. No. 5,399,363 (each specifically incorporated herein by reference in its entirety).

As used herein, "carrier" includes any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

The phrase "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human. The preparation of an aqueous composition that contains a protein as an active ingredient is well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared.

In certain embodiments, the compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, polynucleotides, and peptide compositions directly to the lungs via nasal aerosol sprays has been described e.g., in U.S. Pat. No. 5,756,353 and U.S. Pat. No. 5,804,212 (each specifically incorporated herein by reference in its entirety). Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga et al., 1998) and lysophosphatidyl-glycerol compounds (U.S. Pat. No. 5,725,871, specifically incorporated herein by reference in its entirety) are also well-known in the pharmaceutical arts. Likewise, transmucosal drug delivery in the form of a polytetrafluoroethylene support matrix is described in U.S. Pat. No. 5,780,045 (specifically incorporated herein by reference in its entirety). Particular embodiments of the invention may comprise other formulations, such as those that are well known in the pharmaceutical art, and are described, for example, in Remington: The Science and Practice of Pharmacy, 20th Edition. Baltimore, Md.: Lippincott Williams & Wilkins, 2000.

H. Methods of Delivery

In one embodiment, cells, e.g., stem cells such as satellite stem cells, are contacted with a composition comprising one or more inventive Wnt polypeptides and/or polynucleotides. It is contemplated that the cells of the invention may be contacted in vitro, ex vivo, or in vivo. In other embodiments, the Wnt compositions of the invention are administered to a subject.

The compositions of the invention can be administered (as proteins/polypeptides, or in the context of expression vectors for gene therapy) directly to the subject or delivered ex vivo, to cells derived from the subject (e.g., as in ex vivo gene therapy). Direct in vivo delivery of the compositions will generally be accomplished by parenteral injection, e.g., subcutaneously, intraperitoneally, intravenously myocardial, intratumoral, peritumoral, or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hypodermic sprays.

The compositions of the invention may also be administered by direct injection into a tissue, such as a muscle. In

some embodiments of the invention, a composition of the invention is administered by directly injecting the composition into muscle tissue to prevent a loss of muscle in the injected muscle or to promote regeneration or repair of the injected muscle, for example by promoting expansion of the muscle cells or hypertrophy of the injected muscle.

Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, direct microinjection of the DNA into nuclei, and viral-mediated, such as adenovirus (and adeno-associated virus) or alphavirus, all well known in the art.

In certain embodiments, it will be preferred to deliver one or more modified Wnts using a viral vector or other in vivo polynucleotide delivery technique. In a preferred embodiment, the viral vector is a non-integrating vector or a transposon-based vector. This may be achieved using any of a variety of well-known approaches, such as vectors including adenovirus, retrovirus, lentivirus, adeno-associated virus vectors (AAV), or the use of other viral vectors as expression constructs (including without limitation vaccinia virus, polioviruses and herpes viruses).

Non-viral methods may also be employed for administering the polynucleotides of the invention. In one embodiment, a polynucleotide may be administered directly to a cell via microinjection or a tissue via injection, such as by using techniques described in Dubensky et al., (1984) or Benvenisty & Reshef (1986). It is envisioned that DNA encoding a gene of interest may also be transferred in a similar manner in vivo and express the gene product.

Another embodiment of the invention for transferring a naked DNA expression construct into cells may involve particle bombardment. This method depends on the ability to accelerate DNA-coated microprojectiles to a high velocity allowing them to pierce cell membranes and enter cells without killing them (Klein et al., 1987). In another embodiment, polynucleotides are administered to cells via electroporation.

I. Methods of Treatment

The modified Wnt polypeptides and compositions of the invention are useful for various therapeutic applications. For example, the compositions and methods described herein are useful for promoting tissue formation, regeneration, repair or maintenance in a subject in need thereof.

Some relevant therapeutic applications for the Wnt compositions of the invention include situations where there is a need to prevent muscle loss or regenerate lost or damaged muscle tissue by increasing muscle size, volume or strength. Such situations may include, for example, after chemotherapy or radiation therapy, after muscle injury, or in the treatment or management of diseases and conditions affecting muscle. In certain embodiments, the disease or condition affecting muscle may include a wasting disease (e.g., cachexia, which may be associated with an illness such as cancer or AIDS), muscular attenuation or atrophy, or a muscle degenerative disease. Muscular attenuation and atrophy may be associated with, for example, sarcopenia (including age-related sarcopenia), ICU-induced weakness, disuse of muscle (for example disuse of muscle due to coma paralysis, injury, or immobilization), surgery-induced weakness (e.g., following hip or knee replacement), or a muscle degenerative disease (e.g., muscular dystrophies). This list is not exhaustive.

In certain embodiments, the polypeptides and compositions of the invention may be used to stimulate symmetrical

expansion of muscle satellite cells, thereby increasing the proportion of resident satellite cells, or committed precursor cells, in a muscle tissue. The polypeptides and compositions may also be used to promote muscle hypertrophy, such as by increasing the size of individual muscle fibers. The polypeptides and compositions of the invention may thus increase both the number of muscle cells and the size of muscle cells, and as a result may be useful for example, to replace damaged or defective tissue, or to prevent muscle atrophy or loss of muscle mass, in particular, in relation to diseases and disorders affecting muscle, such as muscular dystrophy, neuro-muscular and neurodegenerative diseases, muscle wasting diseases and conditions, atrophy, cardiovascular disease, stroke, heart failure, myocardial infarction, cancer, HIV infection, AIDS, and the like.

In additional embodiments, the compositions and methods are useful for repairing or regenerating dysfunctional skeletal muscle, for instance, in subjects having muscle degenerative diseases. The subject can be suspected of having, or be at risk of at having skeletal muscle damage, degeneration or atrophy. The skeletal muscle damage may be disease related or non-disease related. The human subject may have or be at risk of having muscle degeneration or muscle wasting. The muscle degeneration or muscle wasting may be caused in whole or in part by a disease, for example aids, cancer, a muscular degenerative disease, or a combination thereof.

Illustrative examples of muscular dystrophies include, but are not limited to Duchenne muscular dystrophy (DMD), Becker muscular dystrophy (BMD), myotonic dystrophy (also known as Steinert's disease), limb-girdle muscular dystrophies, facioscapulohumeral muscular dystrophy (FSH), congenital muscular dystrophies, oculopharyngeal muscular dystrophy (OPMD), distal muscular dystrophies and Emery-Dreifuss muscular dystrophy. See, e.g., Hoffman et al., *N. Engl. J. Med.*, 318:1363-1368 (1988); Bonnemant, C. G. et al., *Curr. Opin. Ped.*, 8: 569-582 (1996); Worton, R., *Science*, 270: 755-756 (1995); Funakoshi, M. et al., *Neuromuscul. Disord.*, 9 (2): 108-114 (1999); Lim, L. E. and Campbell, K. P., *Cure. Opin. Neurol.*, 11 (5): 443-452 (1998); Voit, T., *Brain Dev.*, 20 (2): 65-74 (1998); Brown, R. H., *Annu. Rev. Med.*, 48: 457-466 (1997); Fisher, J. and Upadhyaya, M., *Neuromuscul. Disord.*, 7 (1): 55-62 (1997).

In certain embodiments, a use of a composition as described herein for the manufacture of a medicament for promoting muscle formation, maintenance, repair, or regeneration of muscle in a subject in need thereof is provided. In particular embodiments, a composition as described herein is provided for use in the manufacture of a medicament for promoting muscle formation, maintenance, repair, or regeneration of muscle in a subject in need thereof is provided. The Wnt polypeptides may be used for preventing or treating muscle atrophy, such as by increasing the size or number of myofibers.

The composition may be administered in an effective amount, such as a therapeutically effective amount. For in vivo treatment of human and non-human subjects, the subject is usually administered a composition comprising an effective amount of one or more modified Wnt polypeptides of the present invention. An "effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic or prophylactic result.

A "therapeutically effective amount" of a Wnt polypeptide of the invention, or a composition comprising the same, may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of a Wnt polypeptide to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or

detrimental effects of a Wnt polypeptide are outweighed by the therapeutically beneficial effects. The term "therapeutically effective amount" refers to an amount of a Wnt polypeptide or composition comprising the same that is effective to "treat" a disease or disorder in a mammal (e.g., a patient).

A "prophylactically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired prophylactic result. Typically but not necessarily, since a prophylactic dose is used in subjects prior to or at an earlier stage of disease, the prophylactically effective amount is less than the therapeutically effective amount.

In various embodiments, the invention provides for methods of increasing the division symmetry of adult stem cells, such as satellite stem cells compared to untreated stem cell populations. The methods disclosed herein are further capable of promoting symmetrical stem cell division without altering the rate of stem cell division and can promote the survival of a population of stem cells. The methods may be performed in vitro, ex vivo, or in vivo.

In particular embodiments, compositions comprising one or more modified Wnt polypeptides and/or polynucleotides are administered in vivo to a subject in need thereof. As used herein, the term "subject" includes, but is not limited to, a mammal, including, e.g., a human, non-human primate (e.g., baboon, orangutan, monkey), mouse, pig, cow, goat, dog, cat, rabbit, rat, guinea pig, hamster, horse, monkey, sheep, or other non-human mammal; a non-mammal, including, e.g., a non-mammalian vertebrate, such as a bird (e.g., a chicken or duck) or a fish, and a non-mammalian invertebrate. In preferred embodiments, the subject is human. Subjects in need of treatment for a disease or condition include subjects exhibiting symptoms of such disease or condition, such as those having a disease or condition, as well as those at risk of having a disease or condition.

In particular embodiments, a method for expanding a population of satellite stem cells in vivo, ex vivo, or in vitro comprising contacting the stem cells with an effective amount of a composition comprising a modified non-canonical Wnt polypeptide or a polynucleotide encoding such a modified non-canonical Wnt polypeptide. In particular embodiments, the non-canonical Wnt is selected from the group consisting of: Wnt4, Wnt5a, Wnt5b, Wnt6, Wnt7a, Wnt7b, and Wnt11. In preferred embodiments, the Wnt polypeptide is a Wnt5a or Wnt7a polypeptide or an active fragment or variant thereof, or ortholog, paralog, or homolog thereof, that binds to and activates a Wnt receptor.

Without being bound to any particular theory, it is believed that increasing the number of satellite cells in a tissue, provides enhanced regeneration potential of the tissue.

In particular embodiments, stem cells are isolated or maintained, and expanded ex vivo or in vitro and subsequently administered to a subject in need thereof. For example, stem cells can be cultured and expanded ex vivo or in vitro and contacted with an effective amount of a Wnt composition of the invention and then administered to a patient as a therapeutic stem cell composition according to methods known to skilled persons. In certain embodiments, the expanded stem cell population is administered to the patient in combination with a therapeutic Wnt composition.

The methods of promoting stem cell expansion can be used to stimulate the ex vivo or in vitro expansion of stem cells and thereby provide a population of cells suitable for transplantation or administration to a subject in need thereof.

In some forms of urinary continence, the dysfunctional muscle can be treated with a composition or method of the

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invention, for example, by direct protein injection into the muscle. Thus, in one embodiment, the method is useful for treating urinary incontinence.

In further embodiments, damaged or dysfunctional muscle tissue may be cardiac muscle. For instance, the damaged muscle tissue may be cardiac muscle damaged by a cardiovascular event such as myocardial infarct, or heart failure, where the target stem cell would be a cardiac stem cell. In accordance with another aspect of the present invention, there is provided a method of promoting cardiac stem cell expansion or cardiac muscle hypertrophy in a mammal comprising administering to the mammal an effective amount of a composition as described herein.

Further, in addition to using the stem cells in transplants, stem cells, or compositions comprising stem cells may be used as a research tool and/or as part of a diagnostic assay or kit. Without wishing to be limiting a kit may comprise muscle stem cells, one or more modified Wnt polypeptides, cell culture or growth medium, cell cryopreservation medium, one or more pharmaceutically acceptable delivery media, one or more modified Wnt polynucleotide sequences or genetic constructs, one or more devices for implantation or delivery of cells to a subject in need thereof, instructions for using, delivering, implanting, culturing, cryopreserving or any combination thereof of the cells as described herein.

Indicators of cell expansion and/or muscle hypertrophy may be monitored qualitatively or quantitatively and include, for example, changes in gross morphology, total cell number, histology, histochemistry or immunohistochemistry, or the presence, absence or relative levels of specific cellular markers. The presence, absence or relative levels of cellular markers can be analyzed by, for example, histochemical techniques, immunological techniques, electrophoresis, Western blot analysis, FACS analysis, flow cytometry and the like. Alternatively the presence of mRNA expressed from the gene encoding the cellular marker protein can be detected, for example, using PCR techniques, Northern blot analysis, the use of suitable oligonucleotide probes and the like.

All publications, patent applications, and issued patents cited in this specification are herein incorporated by reference as if each individual publication, patent application, or issued patent were specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to one of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims. The following examples are provided by way of illustration only and not by way of limitation. Those of skill in the art will readily recognize a variety of noncritical parameters that could be changed or modified to yield essentially similar results.

EXAMPLES

Example 1

Wnt Polypeptides have Conserved Sites for Post-Translational Modification

Wnt proteins are secreted signaling proteins involved in cell survival, proliferation, division and migration. Wnts are required for effective tissue patterning during embryogenesis and tissue regeneration in the adult. Certain Wnt proteins

36

drive skeletal muscle regeneration through stimulation of satellite stem cell symmetric expansion and muscle fiber hypertrophy.

19 human Wnts have been identified and grouped based of discrete regions of homology. The Wnt proteins have complex post-translational modifications including both glycosylation and lipidation. Protein glycosylation is required for effective protein folding and secretion. FIG. 1 is an alignment of all 19 human Wnt polypeptides. The amino acid residues modified by either glycosylation or lipidation are well conserved (see shaded residues). Further, these same residues are conserved across species as can be seen from the alignment of Wnt7a polypeptides in FIGS. 2 and 11. Lipidation has historically been thought to be required for effective activity by fixing the mature secreted protein to the plasma membrane; effectively localizing the Wnt to its frizzled receptors. For this reason, Wnts are thought to be autocrine or local paracrine signaling molecules rather than fully systemic growth factor/cytokines.

As described elsewhere herein, protein lipidation is not a requirement for the activity of all Wnt polypeptides. The selective mutation of lipidated cysteine or serine residues in a wild type Wnt (wtWnt) sequence, e.g., Wnt7a, SEQ ID NO: 2, were replaced with non-lipidated alanine residues. In the specific example of Wnt7a, the cysteine residue at position 73 and/or the serine residue at position 206 were mutated to alanine residues. This resulted in proteins comprising the sequences listed in SEQ ID Nos: 3-5, which lacked post translational lipidation at the mutated residues.

Example 2

Non-Canonical Wnts Induce Myoblast Hypertrophy

Wnt polypeptides signal via frizzled receptors and coreceptors to stimulate several intracellular pathways. Wnts are generally categorized as either "canonical" or "non-canonical" signaling molecules where canonical signaling results in the nuclear localization of the protein β -Catenin and subsequent expression of target genes. Non-canonical signaling generally includes cellular functions of Wnts that do not directly involve the nuclear localization of β -Catenin, such as the activation of the planar cell polarity (PCP) or Calcium/PLC/PKC pathways. Receptors and coreceptors for canonical and non-canonical pathway activation are different; with the canonical signaling pathway showing dependence for the co-receptor LRP. Wnt7a is a non-canonical signaling molecule and has been shown to drive symmetrical expansion of muscle satellite stem cells via the activation of the PCP pathway (Le Grand et al., *Wnt7a* activates the planar cell polarity pathway to drive the symmetric expansion of satellite stem cells. *Cell Stem Cell* 4, 535-547, 2009). More recently Wnt7a was shown to drive the hypertrophy of myoblasts in culture, potentially via a G-protein-dependent activation of the PI3-Kinase/mTOR pathway (Julia von Maltzahn, C. Florian Bentzinger and Michael A. Rudnicki, *Nature Cell Biology*, Dec. 11, 2011; *epub*).

The ability of several Wnt polypeptides to induce hypertrophy of myoblast cells was tested. The Wnt polypeptides tested initially were obtained from R&D systems and represented canonical (Wnt3a) and non-canonical (Wnt5a and Wnt7a) signaling polypeptides. As shown in FIG. 3, while buffer control or canonical Wnt polypeptide Wnt3a had no myoblast hypertrophy effect, both non-canonical Wnt polypeptides (Wnt7a and Wnt5a) produced significant myoblast hypertrophy effect in vitro.

Methods

C2C12 mouse myoblasts were obtained from ATCC (#CRL-1772) and grown on gelatin-coated tissue culture plates in DMEM (MediaTech #10-017-CV) medium supplemented with 10% 50 FBS. The cells remained less than 20% confluent throughout the experiment. 96 well tissue culture plates were coated with 0.1% gelatin for at least 15 minutes at room temperature (RT) and 2,000 cells (in 0.2 mL of growth medium) were plated in each well of the 96-well plate. The plates were then incubated for 24 hours at 37° C. The following day, the media was aspirated and replaced with 0.2 mL of a differentiation media having DMEM (MediaTech #10-017-CV) supplemented with 2% horse serum (Fisher, Hyclone SH30074). After 3 days of differentiation, Wnt polypeptides (rhWnt7a #3008-WN/CF, rhWnt3a #5036-WN/CF or rhWnt5a #645-WN/CF (from R&D systems) were added to the cell culture and incubated for an additional 2 days.

The cells were fixed, washed, permeabilized, and stained with myosin slow and fast myosin antibodies (Sigma #M4276-0.2ML, Sigma #M8421-0.2ML). Cells were visualized; myofiber diameter was calculated for 100 fibers per experiment; and the data from 3 independent biological replicates was collated for a total of 300 data points per treatment group. The median fiber diameter for each biological replicate group is shown in FIG. 3. The mean of the median across the three biological replicates for each group was 17.5 µm for medium alone, 18.8 µm (Wnt3a), 27 µm (Wnt7a), 24.6 µm (Wnt5a), and 25.8 µm (insulin growth factor (IGF)). The increase in hypertrophy for cells treated with Wnt7a, Wnt5a and IGF was statistically significant compared with either media control or Wnt3a treatment.

Example 3

Construction and Expression of Modified Wnt7a Polypeptides

Non-canonical Wnts induce muscle satellite stem cell expansion and muscle hypertrophy. Induction of both processes would be of great benefit therapeutically: for the treatment of cachexia, muscle atrophy, and muscular dystrophy. The use of Wnt as a therapeutic requires effective scaled production, and purification and formulation applicable for therapeutic use while retaining the specific Wnt activity and receptor specificity. The post-translational lipidation of Wnt polypeptides represents a potential complication to these requirements of manufacture. Wnts were generally thought to require lipid for effective activity, lipidated proteins are challenging to purify at high concentrations and require the use of detergent formulation for solubility and stability.

To address these challenges, several variants of Wnt7a were constructed. Specifically, the amino acid residues targeted for post-translational lipidation (Cys 73 and Ser206 in Wnt7a) were mutated to Alanine residues using the following molecular biology techniques. The wild type human Wnt7a was PCR amplified using forward primer 5'-GCATGGATC-CACCATGAACCGGAAAGCGCGG-3' (SEQ ID NO: 41) and reverse primer 5'-GCATGCGGCCGCTCACTTG-CACGTGTACATCTCC-3' (SEQ ID NO: 42). The PCR product was inserted into pcDNA3.1(+) vector between the BamHI and Not I sites. The modified Wnt7a constructs were prepared using the QuikChange® site-directed mutagenesis method. The human Wnt7a C73A construct (cysteine at amino acid 73 substituted with alanine) was made using the human wild type Wnt7a as a template with forward primer 5'-ATGGGCTTGGACGAGGCCAGTTTCAGTTCCGC-3' (SEQ ID NO: 43) and reverse primer 5'-GCGGAAC-

GAAACTGGGCCTCGTCCAGGCCCAT-3' (SEQ ID NO: 44). The human Wnt7a S206A construct (serine at amino acid 206 substituted with alanine) was made using the human wild type Wnt7a as a template using forward primer 5'-GTGC-CACGGCGTGGCAGGCTCGTGCACC-3' (SEQ ID NO: 45) and reverse primer 5'-GGTGCACGAGCCTGCCACGC-CGTGGCAC-3' (SEQ ID NO: 46). The human Wnt7a C73A/S206A constructs were made using the reagents for the individual C73A and S206A constructs. Final vector DNA was prepared using Qiagen Endo-free purification kits. The Wnt cDNAs in the pcDNA3 vector were expressed in HEK293 cells for 48-72 hrs. Wnt polypeptides were subsequently purified from the HEK293 culture media by affinity chromatography using an antibody specific for all variants of Wnt7a produced (Antibody: Santa Cruz K15 #26361). Activity of the purified modified Wnt polypeptides was tested using in vitro hypertrophy assay as seen in subsequent examples. A schematic of all Wnt7a constructs built is shown in FIG. 4 (see also SEQ ID NOs: 1, 2, 3, 4, 5, 12 and 13).

Example 4

Heterologous Signal Peptides Improve Wnt Secretion and Production

To improve production, secretion, and solubility of Wnt proteins showing poor secretion from the mammalian culture in HEK293 cells—with the majority of expressed protein remaining within the cell—Wnt fusion polypeptides were constructed in which the endogenous Wnt secretion signal peptide was replaced by the signal peptide of human immunoglobulin G Kappa chain (IgGK) or that of human protein CD33. A schematic of Wnt7a fusion polypeptides comprising heterologous signal peptides is shown in FIG. 4 (see also SEQ ID NOs: 12 and 13).

As shown in FIG. 5, the Wnt fusion polypeptides having heterologous signal peptides performed significantly better than Wnt polypeptides comprising a native signal peptide, when compared for expression and secretion in HEK293 culture.

Example 5

Modified Wnt Polypeptides can be Formulated in the Absence of Detergent and Retain Stability and Activity

Wnt protein production and formulation has traditionally relied on formulation in detergent to retain solubility of these lipidated proteins. The effective therapeutic delivery of a Wnt polypeptide requires formulation in the absence of detergent. Wnt polypeptides without lipidation sites were constructed as described in Example 3, expressed in mammalian culture systems, purified from the culture media, and formulated in 1% CHAPS detergent. A HPLC-based assay was configured to allow the effective measurement of CHAPS detergent in the Wnt polypeptide formulations.

As shown in FIG. 6a, a titration of CHAPS detergent in solution allowed for effective calibration of the assay. Various preparations of pure Wnt polypeptide were tested and final formulation was shown to be ~1% CHAPS solution in PBS (FIG. 6b). Subsequent dialysis of the Wnt polypeptide solution against PBS alone effectively removed the detergent below the level of detection (FIG. 6c). The dialyzed polypeptides were then tested for both stability and activity either in the presence or absence of the CHAPS detergent.

Incubation of the protein formulations at either 4° C. or 37° C. over a 7 day period showed Wnt with native lipidation sites was relatively stable when formulated in detergent but unstable when formulated in the absence of detergent. Conversely, modified Wnts with lipidation sites removed and replaced with Alanine (C73A, S206A) were seen to have improved stability in the absence of detergent when compared to native, lipidated protein.

Wnt variants formulated with or without detergent were then tested for activity in the C2C12 hypertrophy assay as described in Example 2. Wnt polypeptides were produced in HEK293 mammalian culture systems and affinity purified. The Wnt polypeptides were formulated in PBS with 1% CHAPS detergent. Aliquots of each Wnt polypeptides variant were reformulated by detergent removal using dialysis. Wnt proteins had equal molar concentration and were applied to the C2C12 hypertrophy assay.

Wnt polypeptides produced in the HEK293 culture system with the use of heterologous signal peptides retained their activity when compared to a positive control, native Wnt sequence (FIG. 7). Further, Wnt7a C73A and S206A mutants retained specific hypertrophic activity (FIG. 7). All modified Wnt retained activity when formulated in detergent.

When Wnts were reformulated in the absence of detergent, only the modified Wnts comprising Alanine substituted lipidation sites retained activity, whereas native Wnts lost myoblast hypertrophic activity (FIG. 7). Thus, Wnts specifically altered at conserved lipidation sites, retained biological activity. The modified Wnts also retained activity when formulated in the absence of detergent. Accordingly, the modified Wnt polypeptides of the invention represent useful therapeutic versions of the native protein.

Example 6

Modified Wnt7a Increases Muscle Hypertrophy and Satellite Stem Cell Expansion

To demonstrate the ability of delipidated Wnts, e.g., Wnts that have one or more lipidation sites removed, to stimulate muscle regeneration in vivo, the modified Wnt7a were over-expressed by electroporation of CMV-Wnt7a expression plasmids into TA muscles of 3-month old mice.

1. In Vivo Electroporation

Plasmids constructs encoding a LacZ, wild type Wnt7a, Wnt7a C73A, Wnt7a S206A, and Wnt7a C73A/S206A were electroporated in vivo into mice. 40 µg of each plasmid DNA in 0.9% NaCl or 0.9% NaCl (saline) was injected directly into a left TA muscle that had been exposed by an incision through the skin of an anesthetized mouse. Immediately after injection, electric stimulation was applied directly to the TA by a pulse generator (ECM 830, BTX) of 100-150 volts for 6 pulses, with a fixed duration of 20 ms and an interval of 200 ms using 5 mm needle electrodes (BTX). Experimental and contralateral TA muscles were isolated and embedded in OCT-15% Sucrose (Tissue-Tek) and frozen with isopentane cooled by cold nitrogen.

2. Histology and Quantification

Transverse sections (8 µm) of experimental and contralateral muscles were cut with a cryostat (Leica CM1850). The entire TA muscles were sectioned, in order to compare experimental and contralateral muscles at the same level on serial sections (around 400 sections were obtained from each TA muscle). For LacZ reaction, cryosections were fixed with 0.1% glutaraldehyde and exposed to X-gal solution. For H&E and immunostaining, sections were fixed with 4% paraformaldehyde. For enumeration of fibers, pictures of laminin-

stained cryosections were assembled and counted on Adobe Photoshop CS2. Quantification of myofibers caliber was performed with ImageJ. The satellite cell enumeration was performed on Photoshop, on pictures of Pax7 and Laminin co-immunostained cryosections taken in regenerated areas where all the fibers had centrally located nuclei. "Percent Pax-7+ Cells" represents the number of sub-laminar Pax7+ve satellite cells normalized per fiber number, and to the contralateral leg.

3. Statistical Analysis

A minimum of 2 and up to 5 replicates was done for experiments presented. Data are presented as standard error of the mean. Results were assessed for statistical significance using Student's T Test (Microsoft Excel) and differences were considered statistically significant at the p<0.05 level.

4. Results

Electroporation of WT Wnt7a, Wnt7a C73A, Wnt7a S206A, and Wnt7a C73A/S206A constructs produced a statistically significant increase in the average fiber diameter of mouse TA muscles compared to a LacZ control plasmid. Moreover, the Wnt7a C73A, Wnt7a S206A, and Wnt7a C73A/S206A constructs retained Wnt biological activity of the wild type Wnt construct, as the increased the average fiber diameter of the TA muscles produced by the Wnt7a C73A, Wnt7a S206A, and Wnt7a C73A/S206A constructs was comparable to that produced by the wild type Wnt construct. These results are shown in FIG. 1.

Notably, FIG. 2 shows that TA muscles electroporated with Wnt7a S206A and Wnt7a C73A/S206A constructs also exhibited a comparable increase in TA muscle mass to TA muscles electroporated with the wild type Wnt construct.

To assess whether Wnt7a C73A, Wnt7a S206A, and Wnt7a C73A/S206A similarly stimulated the expansion of satellite stem cells in vivo, the numbers of satellite cells and satellite stem cells in regenerated muscle were assessed following electroporation of the modified Wnt7a expression plasmids. Over-expression of Wnt7a C73A, Wnt7a S206A, and Wnt7a C73A/S206A resulted in statistically significant increases in the number of Pax7+ satellite cells per myofiber on sections at 3 weeks after electroporation (Wnt7a C73A, p=0.001, n=4; Wnt7a S206A, p=0.01, n=2; Wnt7a C73A/S206A, p=0.05, n=2). The increase in the number of Pax7 satellite cells induced by over-expression of Wnt7a C73A, Wnt7a S206A, and Wnt7a C73A/S206A was comparable to the increase induced by wild type Wnt7a. These results are shown in FIG. 3.

Taken together, these results shown in FIGS. 1-3 indicate that over-expression of Wnt7a C73A, Wnt7a S206A, and Wnt7a C73A/S206A markedly enhances muscle regeneration, as evidenced by the presence of increased numbers of larger fibers and the increased mass of muscle and further, increases the numbers of satellite stem cells in vivo. In addition, these results show that the effect produced by Wnt7a C73A, Wnt7a S206A, and Wnt7a C73A/S206A was comparable to the effect produced by wild type Wnt7a.

In general, in the following claims, the terms used should not be construed to limit the claims to the specific embodiments disclosed in the specification and the claims, but should be construed to include all possible embodiments along with the full scope of equivalents to which such claims are entitled. Accordingly, the claims are not limited by the disclosure.

Example 7

Wnt Proteins can be Expressed as Immunoglobulin Fc Fusions

Immunoglobulin fusion proteins and/or peptibodies have been used to improve the pharmaceutical properties of the

Wnt polypeptides, such as their circulating half life in vivo. Wnt proteins of the present invention were constructed in mammalian expression vectors (pcDNA3+) with either amino-terminal or carboxyterminal Fc-fusion domains as schematically represented in FIG. 4. Amino acid residues 31-349 of native human Wnt7a or the same with C73A and/or S206A mutations were subcloned in frame with the IgG Kappa secretion signal peptide and Human IgGle3-Fc1 domain as either a N- or C-terminal fusion. This Fc domain comprised amino acid changes that are different from native IgG1 sequence (E233P/L234V/L235A/deltaG236+A327G/A330S/P331S) to reduce antibody dependent cell-mediated cytotoxicity (ADCC) and complement dependent cytotoxic-

ity (CDC) effects. A 17 amino acid linker (GT(GGGGS)3) was added between the Wnt protein sequence and the Fc-fusion sequence to reduce steric hindrance and prevent reduction of Wnt specific activity. These vectors were transfected into HEK293 cells and protein expression continued for 48 hours. Protein expression and secretion was monitored by western blot and can be seen in FIGS. 11a and 11b. Intact fusion proteins of the expected molecular weight were seen when immune-detected with either anti-Wnt7a antibodies or anti-Fc detection. Effective secretion was observed for the fusion proteins. Secreted proteins were subsequently purified by Protein A or Protein G affinity chromatography.

SEQUENCE LISTING

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-continued

<220> FEATURE:

<223> OTHER INFORMATION: Engineered mutation of human Wnt-7A polypeptide

<400> SEQUENCE: 5

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Met Asn Arg Lys Ala Arg Arg Cys Leu Gly His Leu Phe Leu Ser Leu
1      5      10      15
Gly Met Val Tyr Leu Arg Ile Gly Gly Phe Ser Ser Val Val Ala Leu
      20      25      30
Gly Ala Ser Ile Ile Cys Asn Lys Ile Pro Gly Leu Ala Pro Arg Gln
      35      40      45
Arg Ala Ile Cys Gln Ser Arg Pro Asp Ala Ile Ile Val Ile Gly Glu
      50      55      60
Gly Ser Gln Met Gly Leu Asp Glu Ala Gln Phe Gln Phe Arg Asn Gly
      65      70      75      80
Arg Trp Asn Cys Ser Ala Leu Gly Glu Arg Thr Val Phe Gly Lys Glu
      85      90      95
Leu Lys Val Gly Ser Arg Glu Ala Ala Phe Thr Tyr Ala Ile Ile Ala
      100     105     110
Ala Gly Val Ala His Ala Ile Thr Ala Ala Cys Thr Gln Gly Asn Leu
      115     120     125
Ser Asp Cys Gly Cys Asp Lys Glu Lys Gln Gly Gln Tyr His Arg Asp
      130     135     140
Glu Gly Trp Lys Trp Gly Gly Cys Ser Ala Asp Ile Arg Tyr Gly Ile
      145     150     155     160
Gly Phe Ala Lys Val Phe Val Asp Ala Arg Glu Ile Lys Gln Asn Ala
      165     170     175
Arg Thr Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg Lys Ile Leu
      180     185     190
Glu Glu Asn Met Lys Leu Glu Cys Lys Cys His Gly Val Ala Gly Ser
      195     200     205
Cys Thr Thr Lys Thr Cys Trp Thr Thr Leu Pro Gln Phe Arg Glu Leu
      210     215     220
Gly Tyr Val Leu Lys Asp Lys Tyr Asn Glu Ala Val His Val Glu Pro
      225     230     235     240
Val Arg Ala Ser Arg Asn Lys Arg Pro Thr Phe Leu Lys Ile Lys Lys
      245     250     255
Pro Leu Ser Tyr Arg Lys Pro Met Asp Thr Asp Leu Val Tyr Ile Glu
      260     265     270
Lys Ser Pro Asn Tyr Cys Glu Glu Asp Pro Val Thr Gly Ser Val Gly
      275     280     285
Thr Gln Gly Arg Ala Cys Asn Lys Thr Ala Pro Gln Ala Ser Gly Cys
      290     295     300
Asp Leu Met Cys Cys Gly Arg Gly Tyr Asn Thr His Gln Tyr Ala Arg
      305     310     315     320
Val Trp Gln Cys Asn Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys
      325     330     335
Asn Thr Cys Ser Glu Arg Thr Glu Met Tyr Thr Cys Lys
      340     345

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<210> SEQ ID NO 6

<211> LENGTH: 349

<212> TYPE: PRT

<213> ORGANISM: Mus musculus

<400> SEQUENCE: 6

-continued

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Met Thr Arg Lys Ala Arg Arg Cys Leu Gly His Leu Phe Leu Ser Leu
 1          5          10          15

Gly Ile Val Tyr Leu Arg Ile Gly Gly Phe Ser Ser Val Val Ala Leu
      20          25          30

Gly Ala Ser Ile Ile Cys Asn Lys Ile Pro Gly Leu Ala Pro Arg Gln
      35          40          45

Arg Ala Ile Cys Gln Ser Arg Pro Asp Ala Ile Ile Val Ile Gly Glu
      50          55          60

Gly Ser Gln Met Gly Leu Asp Glu Cys Gln Phe Gln Phe Arg Asn Gly
      65          70          75          80

Arg Trp Asn Cys Ser Ala Leu Gly Glu Arg Thr Val Phe Gly Lys Glu
      85          90          95

Leu Lys Val Gly Ser Arg Glu Ala Ala Phe Thr Tyr Ala Ile Ile Ala
      100          105          110

Ala Gly Val Ala His Ala Ile Thr Ala Ala Cys Thr Gln Gly Asn Leu
      115          120          125

Ser Asp Cys Gly Cys Asp Lys Glu Lys Gln Gly Gln Tyr His Arg Asp
      130          135          140

Glu Gly Trp Lys Trp Gly Gly Cys Ser Ala Asp Ile Arg Tyr Gly Ile
      145          150          155          160

Gly Phe Ala Lys Val Phe Val Asp Ala Arg Glu Ile Lys Gln Asn Ala
      165          170          175

Arg Thr Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg Lys Ile Leu
      180          185          190

Glu Glu Asn Met Lys Leu Glu Cys Lys Cys His Gly Val Ser Gly Ser
      195          200          205

Cys Thr Thr Lys Thr Cys Trp Thr Thr Leu Pro Gln Phe Arg Glu Leu
      210          215          220

Gly Tyr Val Leu Lys Asp Lys Tyr Asn Glu Ala Val His Val Glu Pro
      225          230          235          240

Val Arg Ala Ser Arg Asn Lys Arg Pro Thr Phe Leu Lys Ile Lys Lys
      245          250          255

Pro Leu Ser Tyr Arg Lys Pro Met Asp Thr Asp Leu Val Tyr Ile Glu
      260          265          270

Lys Ser Pro Asn Tyr Cys Glu Glu Asp Pro Val Thr Gly Ser Val Gly
      275          280          285

Thr Gln Gly Arg Ala Cys Asn Lys Thr Ala Pro Gln Ala Ser Gly Cys
      290          295          300

Asp Leu Met Cys Cys Gly Arg Gly Tyr Asn Thr His Gln Tyr Ala Arg
      305          310          315          320

Val Trp Gln Cys Asn Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys
      325          330          335

Asn Thr Cys Ser Glu Arg Thr Glu Met Tyr Thr Cys Lys
      340          345

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<210> SEQ ID NO 7

<211> LENGTH: 349

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 7

```

Met Thr Arg Lys Ala Arg Arg Cys Leu Gly His Leu Phe Leu Ser Leu
 1          5          10          15

Gly Ile Val Tyr Leu Arg Ile Gly Asp Phe Ser Ser Val Val Ala Leu
      20          25          30

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-continued

Gly Ala Ser Ile Ile Cys Asn Lys Ile Pro Gly Leu Ala Pro Arg Gln
 35 40 45
 Arg Ala Ile Cys Gln Ser Arg Pro Asp Ala Ile Ile Val Ile Gly Glu
 50 55 60
 Gly Ser Gln Met Gly Leu Asp Glu Cys Gln Phe Gln Phe Arg Asn Gly
 65 70 75 80
 Arg Trp Asn Cys Ser Ala Leu Gly Glu Arg Thr Val Phe Gly Lys Glu
 85 90 95
 Leu Lys Val Gly Ser Arg Glu Ala Ala Phe Thr Tyr Ala Ile Ile Ala
 100 105 110
 Ala Gly Val Ala His Ala Ile Thr Ala Ala Cys Thr Gln Gly Asn Leu
 115 120 125
 Ser Asp Cys Gly Cys Asp Lys Glu Lys Gln Gly Gln Tyr His Arg Asp
 130 135 140
 Glu Gly Trp Lys Trp Gly Gly Cys Ser Ala Asp Ile Arg Tyr Gly Ile
 145 150 155 160
 Gly Phe Ala Lys Val Phe Val Asp Ala Arg Glu Ile Lys Gln Asn Ala
 165 170 175
 Arg Thr Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg Lys Ile Leu
 180 185 190
 Glu Glu Asn Met Lys Leu Glu Cys Lys Cys His Gly Val Ser Gly Ser
 195 200 205
 Cys Thr Thr Lys Thr Cys Trp Thr Thr Leu Pro Gln Phe Arg Glu Leu
 210 215 220
 Gly Tyr Val Leu Lys Asp Lys Tyr Asn Glu Ala Val His Val Glu Pro
 225 230 235 240
 Val Arg Ala Ser Arg Asn Lys Arg Pro Thr Phe Leu Lys Ile Lys Lys
 245 250 255
 Pro Leu Ser Tyr Arg Lys Pro Met Asp Thr Asp Leu Val Tyr Ile Glu
 260 265 270
 Lys Ser Pro Asn Tyr Cys Glu Glu Asp Pro Val Thr Gly Ser Val Gly
 275 280 285
 Thr Gln Gly Arg Ala Cys Asn Lys Thr Ala Pro Gln Ala Ser Gly Cys
 290 295 300
 Asp Leu Met Cys Cys Gly Arg Gly Tyr Asn Thr His Gln Tyr Ala Arg
 305 310 315 320
 Val Trp Gln Cys Asn Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys
 325 330 335
 Asn Thr Cys Ser Glu Arg Thr Glu Met Tyr Thr Cys Lys
 340 345

<210> SEQ ID NO 8
 <211> LENGTH: 349
 <212> TYPE: PRT
 <213> ORGANISM: Gallus gallus

<400> SEQUENCE: 8

Met Asn Arg Lys Thr Arg Arg Trp Ile Phe His Ile Phe Leu Ser Leu
 1 5 10 15
 Gly Ile Val Tyr Ile Lys Ile Gly Gly Phe Ser Ser Val Val Ala Leu
 20 25 30
 Gly Ala Ser Ile Ile Cys Asn Lys Ile Pro Gly Leu Ala Pro Arg Gln
 35 40 45
 Arg Ala Ile Cys Gln Ser Arg Pro Asp Ala Ile Ile Val Ile Gly Glu

-continued

50	55	60
Gly Ser Gln Met Gly Ile Asn Glu Cys Gln Phe Gln Phe Arg Asn Gly		
65	70	75 80
Arg Trp Asn Cys Ser Ala Leu Gly Glu Arg Thr Val Phe Gly Lys Glu		
	85	90 95
Leu Lys Val Gly Ser Arg Glu Ala Ala Phe Thr Tyr Ala Ile Ile Ala		
	100	105 110
Ala Gly Val Ala His Ala Ile Thr Ala Ala Cys Thr Gln Gly Asn Leu		
	115	120 125
Ser Asp Cys Gly Cys Asp Lys Glu Lys Gln Gly Gln Tyr His Lys Glu		
	130	135 140
Glu Gly Trp Lys Trp Gly Gly Cys Ser Ala Asp Ile Arg Tyr Gly Ile		
	145	150 155 160
Gly Phe Ala Lys Val Phe Val Asp Ala Arg Glu Ile Lys Gln Asn Ala		
	165	170 175
Arg Thr Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg Lys Ile Leu		
	180	185 190
Glu Glu Asn Met Lys Leu Glu Cys Lys Cys His Gly Val Ser Gly Ser		
	195	200 205
Cys Thr Thr Lys Thr Cys Trp Thr Thr Leu Pro Lys Phe Arg Glu Leu		
	210	215 220
Gly Tyr Ile Leu Lys Asp Lys Tyr Asn Glu Ala Val Gln Val Glu Pro		
	225	230 235 240
Val Arg Ala Ser Arg Asn Lys Arg Pro Thr Phe Leu Lys Ile Lys Lys		
	245	250 255
Pro Leu Ser Tyr Arg Lys Pro Met Asp Thr Asp Leu Val Tyr Ile Glu		
	260	265 270
Lys Ser Pro Asn Tyr Cys Glu Glu Asp Pro Val Thr Gly Ser Val Gly		
	275	280 285
Thr Gln Gly Arg Met Cys Asn Lys Thr Ala Gln Gln Ser Asn Gly Cys		
	290	295 300
Asp Leu Met Cys Cys Gly Arg Gly Tyr Asn Thr His Gln Tyr Ser Arg		
	305	310 315 320
Val Trp Gln Cys Asn Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys		
	325	330 335
Asn Thr Cys Ser Glu Arg Thr Glu Val Tyr Thr Cys Lys		
	340	345

<210> SEQ ID NO 9

<211> LENGTH: 349

<212> TYPE: PRT

<213> ORGANISM: Danio rerio

<400> SEQUENCE: 9

Met Ser Arg Lys Thr Arg Arg Trp Ile Phe His Ile Phe Leu Cys Leu		
1	5	10 15
Gly Ile Ile Tyr Leu Lys Ile Gly Gly Phe Ser Ser Val Val Ala Leu		
	20	25 30
Gly Ala Ser Ile Ile Cys Asn Lys Ile Pro Gly Leu Ala Pro Arg Gln		
	35	40 45
Arg Thr Ile Cys Gln Ser Arg Pro Asp Ala Ile Ile Val Ile Gly Glu		
	50	55 60
Gly Ala Gln Met Gly Ile Asn Glu Cys Gln Phe Gln Phe Lys Asn Gly		
65	70	75 80

Arg	Trp	Asn	Cys	Ser	Ala	Leu	Gly	Glu	Arg	Thr	Val	Phe	Gly	Lys	Glu
				85					90					95	
Leu	Lys	Val	Gly	Ser	Lys	Glu	Ala	Ala	Phe	Thr	Tyr	Ala	Ile	Ile	Ala
			100					105					110		
Ala	Gly	Val	Ala	His	Ala	Ile	Thr	Ala	Ala	Cys	Thr	Gln	Gly	Thr	Leu
			115				120					125			
Ser	Gly	Cys	Gly	Cys	Asp	Lys	Glu	Lys	Gln	Gly	Phe	Tyr	Asn	Gln	Glu
			130			135					140				
Glu	Gly	Trp	Lys	Trp	Gly	Gly	Cys	Ser	Ala	Asp	Ile	Arg	Tyr	Gly	Leu
145					150					155					160
Ser	Phe	Ser	Lys	Val	Phe	Leu	Asp	Ala	Arg	Glu	Ile	Lys	Gln	Asn	Ala
				165					170					175	
Arg	Thr	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Val	Gly	Arg	Lys	Ile	Leu
				180				185					190		
Glu	Lys	Asn	Met	Arg	Leu	Glu	Cys	Lys	Cys	His	Gly	Val	Ser	Gly	Ser
				195			200					205			
Cys	Thr	Thr	Lys	Thr	Cys	Trp	Thr	Thr	Leu	Pro	Lys	Phe	Arg	Gln	Leu
						215					220				
Gly	Tyr	Ile	Leu	Lys	Glu	Arg	Tyr	Asn	His	Ala	Val	His	Val	Glu	Pro
225					230					235					240
Val	Arg	Ala	Ser	Arg	Asn	Lys	Arg	Pro	Ala	Phe	Leu	Lys	Val	Lys	Lys
				245					250					255	
Pro	Tyr	Ser	Tyr	Arg	Lys	Pro	Met	Asp	Thr	Asp	Leu	Val	Tyr	Ile	Glu
				260				265					270		
Lys	Ser	Pro	Asn	Tyr	Cys	Glu	Ala	Asp	Pro	Val	Thr	Gly	Ser	Met	Gly
				275			280					285			
Thr	Gln	Gly	Arg	Ile	Cys	Asn	Lys	Thr	Ala	Gln	His	Thr	Asn	Gly	Cys
						295					300				
Asp	Leu	Met	Cys	Cys	Gly	Arg	Gly	Tyr	Asn	Thr	His	Gln	Tyr	Ser	Arg
305					310					315					320
Val	Trp	Gln	Cys	Asn	Cys	Lys	Phe	Leu	Trp	Cys	Cys	Tyr	Val	Lys	Cys
				325					330					335	
Asn	Thr	Cys	Ser	Glu	Arg	Thr	Glu	Val	Tyr	Thr	Cys	Lys			
			340					345							

<400> SEQUENCE: 10

Met 1	Asn	Arg	Lys	Ala 5	Arg	Arg	Cys	Leu	Gly 10	His	Leu	Phe	Leu	Ser 15	Leu
Gly	Leu	Val	Tyr 20	Leu	Arg	Ile	Gly	Gly 25	Phe	Ser	Ser	Val	Val 30	Ala	Leu
Gly	Ala	Ser	Ile	Ile	Cys	Asn	Lys 40	Ile	Pro	Gly	Leu	Ala 45	Pro	Arg	Gln
Arg	Ala 50	Ile	Cys	Gln	Ser	Arg 55	Pro	Asp	Ala	Ile	Ile 60	Val	Ile	Gly	Glu
Gly 65	Ser	Gln	Met	Gly	Leu 70	Asp	Glu	Cys	Gln	Phe 75	Gln	Phe	Arg	Asn 80	Gly
Arg	Trp	Asn	Cys	Ser 85	Ala	Leu	Gly	Glu	Arg 90	Thr	Val	Phe	Gly	Lys 95	Glu
Leu	Lys	Val	Gly 100	Ser	Arg	Glu	Ala	Ala 105	Phe	Thr	Tyr	Ala 110	Ile	Ile	Ala

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Ala Gly Val Ala His Ala Ile Thr Ala Ala Cys Thr Gln Gly Asn Leu
115 120 125

Ser Asp Cys Gly Cys Asp Lys Glu Lys Gln Gly Gln Tyr His Arg Asp
130 135 140

Glu Gly Trp Lys Trp Gly Gly Cys Ser Ala Asp Ile Arg Tyr Gly Ile
145 150 155 160

Gly Phe Ala Lys Val Phe Val Asp Ala Arg Glu Ile Lys Gln Asn Ala
165 170 175

Arg Thr Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg Lys Ile Leu
180 185 190

Glu Glu Asn Met Lys Leu Glu Cys Lys Cys His Gly Val Ser Gly Ser
195 200 205

Cys Thr Thr Lys Thr Cys Trp Thr Thr Leu Pro Gln Phe Arg Glu Leu
210 215 220

Gly Tyr Val Leu Lys Asp Lys Tyr Asn Glu Ala Val His Val Glu Pro
225 230 235 240

Val Arg Ala Ser Arg Asn Lys Arg Pro Thr Phe Leu Lys Ile Lys Lys
245 250 255

Pro Leu Ser Tyr Arg Lys Pro Met Asp Thr Asp Leu Val Tyr Ile Glu
260 265 270

Lys Ser Pro Asn Tyr Cys Glu Glu Asp Pro Val Thr Gly Ser Val Gly
275 280 285

Thr Gln Gly Arg Ala Cys Asn Lys Thr Ala Pro Gln Ala Ser Gly Cys
290 295 300

Asp Leu Met Cys Cys Gly Arg Gly Tyr Asn Thr His Gln Tyr Ala Arg
305 310 315 320

Val Trp Gln Cys Asn Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys
325 330 335

Asn Thr Cys Ser Glu Arg Thr Glu Val Tyr Thr Cys Lys
340 345

<210> SEQ ID NO 11

<211> LENGTH: 349

<212> TYPE: PRT

<213> ORGANISM: Bos taurus

<400> SEQUENCE: 11

Met Asn Arg Lys Ala Arg Arg Cys Leu Gly His Leu Phe Leu Ser Leu
1 5 10 15

Gly Met Val Tyr Leu Arg Ile Gly Gly Phe Ser Ser Val Val Ala Leu
20 25 30

Gly Ala Ser Ile Ile Cys Asn Lys Ile Pro Gly Leu Ala Pro Arg Gln
35 40 45

Arg Ala Ile Cys Gln Ser Arg Pro Asp Ala Ile Ile Val Ile Gly Glu
50 55 60

Gly Ser Gln Met Gly Leu Asp Glu Cys Gln Phe Gln Phe Arg Asn Gly
65 70 75 80

Arg Trp Asn Cys Ser Ala Leu Gly Glu Arg Thr Val Phe Gly Lys Glu
85 90 95

Leu Lys Val Gly Ser Arg Glu Ala Ala Phe Thr Tyr Ala Ile Ile Ala
100 105 110

Ala Gly Val Ala His Ala Ile Thr Ala Ala Cys Thr Gln Gly Asn Leu
115 120 125

Ser Asp Cys Gly Cys Asp Lys Glu Lys Gln Gly Gln Tyr His Arg Asp

-continued

130	135	140
Glu Gly Trp Lys Trp Gly Gly Cys Ser Ala Asp Ile Arg Tyr Gly Ile		
145	150	155
Gly Phe Ala Lys Val Phe Val Asp Ala Arg Glu Ile Lys Gln Asn Ala		
	165	170
Arg Thr Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg Lys Ile Leu		
	180	185
Glu Glu Asn Met Lys Leu Glu Cys Lys Cys His Gly Val Ser Gly Ser		
	195	200
Cys Thr Thr Lys Thr Cys Trp Thr Thr Leu Pro Gln Phe Arg Glu Leu		
	210	215
Gly Tyr Val Leu Lys Asp Lys Tyr Asn Glu Ala Val His Val Glu Pro		
	225	230
Val Arg Ala Ser Arg Asn Lys Arg Pro Ala Phe Leu Lys Ile Lys Lys		
	245	250
Pro Leu Ser Tyr Arg Lys Pro Met Asp Thr Glu Leu Val Tyr Ile Glu		
	260	265
Lys Ser Pro Ser Tyr Cys Glu Glu Asp Pro Ala Thr Gly Ser Val Gly		
	275	280
Thr Gln Gly Arg Ala Cys Asn Lys Thr Ala Pro Gln Ala Ser Gly Cys		
	290	295
Asp Leu Met Cys Cys Gly Arg Gly Tyr Asn Thr His Gln Tyr Ala Arg		
	305	310
Val Trp Gln Cys Asn Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys		
	325	330
Asn Thr Cys Ser Glu Arg Thr Glu Val Tyr Thr Cys Lys		
	340	345
<210> SEQ ID NO 12		
<211> LENGTH: 353		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Human Wnt7a polypeptide with signal peptide of human immunoglobulin kappa chain		
<400> SEQUENCE: 12		
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro		
1	5	10
Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr		
	20	25
Lys Leu Ala Leu Gly Ala Ser Ile Ile Cys Asn Lys Ile Pro Gly Leu		
	35	40
Ala Pro Arg Gln Arg Ala Ile Cys Gln Ser Arg Pro Asp Ala Ile Ile		
	50	55
Val Ile Gly Glu Gly Ser Gln Met Gly Leu Asp Glu Cys Gln Phe Gln		
	65	70
Phe Arg Asn Gly Arg Trp Asn Cys Ser Ala Leu Gly Glu Arg Thr Val		
	85	90
Phe Gly Lys Glu Leu Lys Val Gly Ser Arg Glu Ala Ala Phe Thr Tyr		
	100	105
Ala Ile Ile Ala Ala Gly Val Ala His Ala Ile Thr Ala Ala Cys Thr		
	115	120
Gln Gly Asn Leu Ser Asp Cys Gly Cys Asp Lys Glu Lys Gln Gly Gln		
	130	135
		140

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Tyr His Arg Asp Glu Gly Trp Lys Trp Gly Gly Cys Ser Ala Asp Ile
 145 150 155 160
 Arg Tyr Gly Ile Gly Phe Ala Lys Val Phe Val Asp Ala Arg Glu Ile
 165 170 175
 Lys Gln Asn Ala Arg Thr Leu Met Asn Leu His Asn Asn Glu Ala Gly
 180 185 190
 Arg Lys Ile Leu Glu Glu Asn Met Lys Leu Glu Cys Lys Cys His Gly
 195 200 205
 Val Ser Gly Ser Cys Thr Thr Lys Thr Cys Trp Thr Thr Leu Pro Gln
 210 215 220
 Phe Arg Glu Leu Gly Tyr Val Leu Lys Asp Lys Tyr Asn Glu Ala Val
 225 230 235 240
 His Val Glu Pro Val Arg Ala Ser Arg Asn Lys Arg Pro Thr Phe Leu
 245 250 255
 Lys Ile Lys Lys Pro Leu Ser Tyr Arg Lys Pro Met Asp Thr Asp Leu
 260 265 270
 Val Tyr Ile Glu Lys Ser Pro Asn Tyr Cys Glu Glu Asp Pro Val Thr
 275 280 285
 Gly Ser Val Gly Thr Gln Gly Arg Ala Cys Asn Lys Thr Ala Pro Gln
 290 295 300
 Ala Ser Gly Cys Asp Leu Met Cys Cys Gly Arg Gly Tyr Asn Thr His
 305 310 315 320
 Gln Tyr Ala Arg Val Trp Gln Cys Asn Cys Lys Phe His Trp Cys Cys
 325 330 335
 Tyr Val Lys Cys Asn Thr Cys Ser Glu Arg Thr Glu Met Tyr Thr Cys
 340 345 350

Lys

<210> SEQ ID NO 13

<211> LENGTH: 353

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Modified human Wnt7a polypeptide with signal peptide of human immunoglobulin kappa chain

<400> SEQUENCE: 13

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr
 20 25 30
 Lys Leu Ala Leu Gly Ala Ser Ile Ile Cys Asn Lys Ile Pro Gly Leu
 35 40 45
 Ala Pro Arg Gln Arg Ala Ile Cys Gln Ser Arg Pro Asp Ala Ile Ile
 50 55 60
 Val Ile Gly Glu Gly Ser Gln Met Gly Leu Asp Glu Ala Gln Phe Gln
 65 70 75 80
 Phe Arg Asn Gly Arg Trp Asn Cys Ser Ala Leu Gly Glu Arg Thr Val
 85 90 95
 Phe Gly Lys Glu Leu Lys Val Gly Ser Arg Glu Ala Ala Phe Thr Tyr
 100 105 110
 Ala Ile Ile Ala Ala Gly Val Ala His Ala Ile Thr Ala Ala Cys Thr
 115 120 125
 Gln Gly Asn Leu Ser Asp Cys Gly Cys Asp Lys Glu Lys Gln Gly Gln
 130 135 140

-continued

Tyr His Arg Asp Glu Gly Trp Lys Trp Gly Gly Cys Ser Ala Asp Ile
 145 150 155 160
 Arg Tyr Gly Ile Gly Phe Ala Lys Val Phe Val Asp Ala Arg Glu Ile
 165 170 175
 Lys Gln Asn Ala Arg Thr Leu Met Asn Leu His Asn Asn Glu Ala Gly
 180 185 190
 Arg Lys Ile Leu Glu Glu Asn Met Lys Leu Glu Cys Lys Cys His Gly
 195 200 205
 Val Ala Gly Ser Cys Thr Thr Lys Thr Cys Trp Thr Thr Leu Pro Gln
 210 215 220
 Phe Arg Glu Leu Gly Tyr Val Leu Lys Asp Lys Tyr Asn Glu Ala Val
 225 230 235 240
 His Val Glu Pro Val Arg Ala Ser Arg Asn Lys Arg Pro Thr Phe Leu
 245 250 255
 Lys Ile Lys Lys Pro Leu Ser Tyr Arg Lys Pro Met Asp Thr Asp Leu
 260 265 270
 Val Tyr Ile Glu Lys Ser Pro Asn Tyr Cys Glu Glu Asp Pro Val Thr
 275 280 285
 Gly Ser Val Gly Thr Gln Gly Arg Ala Cys Asn Lys Thr Ala Pro Gln
 290 295 300
 Ala Ser Gly Cys Asp Leu Met Cys Cys Gly Arg Gly Tyr Asn Thr His
 305 310 315 320
 Gln Tyr Ala Arg Val Trp Gln Cys Asn Cys Lys Phe His Trp Cys Cys
 325 330 335
 Tyr Val Lys Cys Asn Thr Cys Ser Glu Arg Thr Glu Met Tyr Thr Cys
 340 345 350

Lys

<210> SEQ ID NO 14
 <211> LENGTH: 1143
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

atgaagaagt ccattggaat attaagccca ggagttgctt tggggatggc tggaagtgca	60
atgtcttcca agttcttct agtggctttg gccatatttt tctccttcgc ccaggttgta	120
attgaagcca attcttggtg gtcgctaggt atgaataacc ctgttcagat gtcagaagta	180
tatattatag gaggcacagcc tctctgcagc caactggcag gactttctca aggacagaag	240
aaactgtgcc acttgatca ggaccacatg cagtacatcg gagaaggcgc gaagacaggc	300
atcaaagaat gccagtatca attccgacat cgaagggtgga actgcagcac tgtggataac	360
acctctgttt ttggcagggt gatgcagata ggcagccgcg agacggcctt cacatacgcg	420
gtgagcgcag caggggtggt gaacgccatg agccgggcgt gccgcgaggg cgagctgtcc	480
acctgcggct gcagccgcgc cgcgcgcccc aaggacctgc cgcgggactg gctctggggc	540
ggctgcggcg acaacatoga ctatggctac cgctttgcca aggagttcgt ggacgcccgc	600
gagcgggagc gcatccacgc caagggtccc tacgagagtg ctgcatacct catgaacctg	660
cacaacaacg aggcgggcgc caggacggtg tacaacctgg ctgatgtggc ctgcaagtgc	720
catgggggtg ccggtcatg tagcctgaag acatgctggc tgcagctggc agacttcgcg	780
aaggtgggtg atgccctgaa ggagaagtac gacagcgcgc cggccatgcg gctcaacagc	840
cggggcaagt tggtagaggt caacagccgc ttcaactcgc ccaccacaca agacctggct	900

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tacatcgacc ccagccctga ctactgcgtg cgcaatgaga gcaccggctc gctgggcacg	960
cagggccgcc tgtgcaacaa gacgtcggag ggcattggatg gctgcgagct catgtgctgc	1020
ggccgtggct acgaccagtt caagaccgtg cagacggagc gctgccactg caagttccac	1080
tggtgctgct acgtcaagtg caagaagtgc acggagatcg tggaccagtt tgtgtgcaag	1140
tag	1143

<210> SEQ ID NO 15
 <211> LENGTH: 380
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

Met Lys Lys Ser Ile Gly Ile Leu Ser Pro Gly Val Ala Leu Gly Met	1 5 10 15
Ala Gly Ser Ala Met Ser Ser Lys Phe Phe Leu Val Ala Leu Ala Ile	20 25 30
Phe Phe Ser Phe Ala Gln Val Val Ile Glu Ala Asn Ser Trp Trp Ser	35 40 45
Leu Gly Met Asn Asn Pro Val Gln Met Ser Glu Val Tyr Ile Ile Gly	50 55 60
Ala Gln Pro Leu Cys Ser Gln Leu Ala Gly Leu Ser Gln Gly Gln Lys	65 70 75 80
Lys Leu Cys His Leu Tyr Gln Asp His Met Gln Tyr Ile Gly Glu Gly	85 90 95
Ala Lys Thr Gly Ile Lys Glu Cys Gln Tyr Gln Phe Arg His Arg Arg	100 105 110
Trp Asn Cys Ser Thr Val Asp Asn Thr Ser Val Phe Gly Arg Val Met	115 120 125
Gln Ile Gly Ser Arg Glu Thr Ala Phe Thr Tyr Ala Val Ser Ala Ala	130 135 140
Gly Val Val Asn Ala Met Ser Arg Ala Cys Arg Glu Gly Glu Leu Ser	145 150 155 160
Thr Cys Gly Cys Ser Arg Ala Ala Arg Pro Lys Asp Leu Pro Arg Asp	165 170 175
Trp Leu Trp Gly Gly Cys Gly Asp Asn Ile Asp Tyr Gly Tyr Arg Phe	180 185 190
Ala Lys Glu Phe Val Asp Ala Arg Glu Arg Glu Arg Ile His Ala Lys	195 200 205
Gly Ser Tyr Glu Ser Ala Arg Ile Leu Met Asn Leu His Asn Asn Glu	210 215 220
Ala Gly Arg Arg Thr Val Tyr Asn Leu Ala Asp Val Ala Cys Lys Cys	225 230 235 240
His Gly Val Ser Gly Ser Cys Ser Leu Lys Thr Cys Trp Leu Gln Leu	245 250 255
Ala Asp Phe Arg Lys Val Gly Asp Ala Leu Lys Glu Lys Tyr Asp Ser	260 265 270
Ala Ala Ala Met Arg Leu Asn Ser Arg Gly Lys Leu Val Gln Val Asn	275 280 285
Ser Arg Phe Asn Ser Pro Thr Thr Gln Asp Leu Val Tyr Ile Asp Pro	290 295 300
Ser Pro Asp Tyr Cys Val Arg Asn Glu Ser Thr Gly Ser Leu Gly Thr	305 310 315 320
Gln Gly Arg Leu Cys Asn Lys Thr Ser Glu Gly Met Asp Gly Cys Glu	

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	325		330		335
Leu Met Cys Cys Gly Arg Gly Tyr Asp Gln Phe Lys Thr Val Gln Thr					
	340		345		350
Glu Arg Cys His Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys Lys					
	355		360		365
Lys Cys Thr Glu Ile Val Asp Gln Phe Val Cys Lys					
	370		375		380

<210> SEQ ID NO 16
 <211> LENGTH: 380
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Mutated human Wnt5a polypeptide

<400> SEQUENCE: 16

Met Lys Lys Ser Ile Gly Ile Leu Ser Pro Gly Val Ala Leu Gly Met	
1 5 10 15	
Ala Gly Ser Ala Met Ser Ser Lys Phe Phe Leu Val Ala Leu Ala Ile	
20 25 30	
Phe Phe Ser Phe Ala Gln Val Val Ile Glu Ala Asn Ser Trp Trp Ser	
35 40 45	
Leu Gly Met Asn Asn Pro Val Gln Met Ser Glu Val Tyr Ile Ile Gly	
50 55 60	
Ala Gln Pro Leu Cys Ser Gln Leu Ala Gly Leu Ser Gln Gly Gln Lys	
65 70 75 80	
Lys Leu Cys His Leu Tyr Gln Asp His Met Gln Tyr Ile Gly Glu Gly	
85 90 95	
Ala Lys Thr Gly Ile Lys Glu Ala Gln Tyr Gln Phe Arg His Arg Arg	
100 105 110	
Trp Asn Cys Ser Thr Val Asp Asn Thr Ser Val Phe Gly Arg Val Met	
115 120 125	
Gln Ile Gly Ser Arg Glu Thr Ala Phe Thr Tyr Ala Val Ser Ala Ala	
130 135 140	
Gly Val Val Asn Ala Met Ser Arg Ala Cys Arg Glu Gly Glu Leu Ser	
145 150 155 160	
Thr Cys Gly Cys Ser Arg Ala Ala Arg Pro Lys Asp Leu Pro Arg Asp	
165 170 175	
Trp Leu Trp Gly Gly Cys Gly Asp Asn Ile Asp Tyr Gly Tyr Arg Phe	
180 185 190	
Ala Lys Glu Phe Val Asp Ala Arg Glu Arg Glu Arg Ile His Ala Lys	
195 200 205	
Gly Ser Tyr Glu Ser Ala Arg Ile Leu Met Asn Leu His Asn Asn Glu	
210 215 220	
Ala Gly Arg Arg Thr Val Tyr Asn Leu Ala Asp Val Ala Cys Lys Cys	
225 230 235 240	
His Gly Val Ser Gly Ser Cys Ser Leu Lys Thr Cys Trp Leu Gln Leu	
245 250 255	
Ala Asp Phe Arg Lys Val Gly Asp Ala Leu Lys Glu Lys Tyr Asp Ser	
260 265 270	
Ala Ala Ala Met Arg Leu Asn Ser Arg Gly Lys Leu Val Gln Val Asn	
275 280 285	
Ser Arg Phe Asn Ser Pro Thr Thr Gln Asp Leu Val Tyr Ile Asp Pro	
290 295 300	
Ser Pro Asp Tyr Cys Val Arg Asn Glu Ser Thr Gly Ser Leu Gly Thr	

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305	310	315	320
Gln Gly Arg Leu Cys Asn Lys Thr Ser Glu Gly Met Asp Gly Cys Glu			
	325	330	335
Leu Met Cys Cys Gly Arg Gly Tyr Asp Gln Phe Lys Thr Val Gln Thr			
	340	345	350
Glu Arg Cys His Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys Lys			
	355	360	365
Lys Cys Thr Glu Ile Val Asp Gln Phe Val Cys Lys			
	370	375	380

<210> SEQ ID NO 17

<211> LENGTH: 380

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Mutated human Wnt5a polypeptide

<400> SEQUENCE: 17

Met Lys Lys Ser Ile Gly Ile Leu Ser Pro Gly Val Ala Leu Gly Met			
1	5	10	15
Ala Gly Ser Ala Met Ser Ser Lys Phe Phe Leu Val Ala Leu Ala Ile			
	20	25	30
Phe Phe Ser Phe Ala Gln Val Val Ile Glu Ala Asn Ser Trp Trp Ser			
	35	40	45
Leu Gly Met Asn Asn Pro Val Gln Met Ser Glu Val Tyr Ile Ile Gly			
	50	55	60
Ala Gln Pro Leu Cys Ser Gln Leu Ala Gly Leu Ser Gln Gly Gln Lys			
	65	70	75
Lys Leu Cys His Leu Tyr Gln Asp His Met Gln Tyr Ile Gly Glu Gly			
	85	90	95
Ala Lys Thr Gly Ile Lys Glu Cys Gln Tyr Gln Phe Arg His Arg Arg			
	100	105	110
Trp Asn Cys Ser Thr Val Asp Asn Thr Ser Val Phe Gly Arg Val Met			
	115	120	125
Gln Ile Gly Ser Arg Glu Thr Ala Phe Thr Tyr Ala Val Ser Ala Ala			
	130	135	140
Gly Val Val Asn Ala Met Ser Arg Ala Cys Arg Glu Gly Glu Leu Ser			
	145	150	155
Thr Cys Gly Cys Ser Arg Ala Ala Arg Pro Lys Asp Leu Pro Arg Asp			
	165	170	175
Trp Leu Trp Gly Gly Cys Gly Asp Asn Ile Asp Tyr Gly Tyr Arg Phe			
	180	185	190
Ala Lys Glu Phe Val Asp Ala Arg Glu Arg Glu Arg Ile His Ala Lys			
	195	200	205
Gly Ser Tyr Glu Ser Ala Arg Ile Leu Met Asn Leu His Asn Asn Glu			
	210	215	220
Ala Gly Arg Arg Thr Val Tyr Asn Leu Ala Asp Val Ala Cys Lys Cys			
	225	230	235
His Gly Val Ala Gly Ser Cys Ser Leu Lys Thr Cys Trp Leu Gln Leu			
	245	250	255
Ala Asp Phe Arg Lys Val Gly Asp Ala Leu Lys Glu Lys Tyr Asp Ser			
	260	265	270
Ala Ala Ala Met Arg Leu Asn Ser Arg Gly Lys Leu Val Gln Val Asn			
	275	280	285
Ser Arg Phe Asn Ser Pro Thr Thr Gln Asp Leu Val Tyr Ile Asp Pro			

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290	295	300
Ser Pro Asp Tyr Cys Val Arg Asn Glu Ser Thr Gly Ser Leu Gly Thr		
305	310	315 320
Gln Gly Arg Leu Cys Asn Lys Thr Ser Glu Gly Met Asp Gly Cys Glu		
	325	330 335
Leu Met Cys Cys Gly Arg Gly Tyr Asp Gln Phe Lys Thr Val Gln Thr		
	340	345 350
Glu Arg Cys His Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys Lys		
	355	360 365
Lys Cys Thr Glu Ile Val Asp Gln Phe Val Cys Lys		
	370	375 380
<210> SEQ ID NO 18		
<211> LENGTH: 380		
<212> TYPE: PRT		
<213> ORGANISM: Artificial Sequence		
<220> FEATURE:		
<223> OTHER INFORMATION: Mutated human Wnt5a polypeptide		
<400> SEQUENCE: 18		
Met Lys Lys Ser Ile Gly Ile Leu Ser Pro Gly Val Ala Leu Gly Met		
1	5	10 15
Ala Gly Ser Ala Met Ser Ser Lys Phe Phe Leu Val Ala Leu Ala Ile		
	20	25 30
Phe Phe Ser Phe Ala Gln Val Val Ile Glu Ala Asn Ser Trp Trp Ser		
	35	40 45
Leu Gly Met Asn Asn Pro Val Gln Met Ser Glu Val Tyr Ile Ile Gly		
	50	55 60
Ala Gln Pro Leu Cys Ser Gln Leu Ala Gly Leu Ser Gln Gly Gln Lys		
	65	70 75 80
Lys Leu Cys His Leu Tyr Gln Asp His Met Gln Tyr Ile Gly Glu Gly		
	85	90 95
Ala Lys Thr Gly Ile Lys Glu Ala Gln Tyr Gln Phe Arg His Arg Arg		
	100	105 110
Trp Asn Cys Ser Thr Val Asp Asn Thr Ser Val Phe Gly Arg Val Met		
	115	120 125
Gln Ile Gly Ser Arg Glu Thr Ala Phe Thr Tyr Ala Val Ser Ala Ala		
	130	135 140
Gly Val Val Asn Ala Met Ser Arg Ala Cys Arg Glu Gly Glu Leu Ser		
	145	150 155 160
Thr Cys Gly Cys Ser Arg Ala Ala Arg Pro Lys Asp Leu Pro Arg Asp		
	165	170 175
Trp Leu Trp Gly Gly Cys Gly Asp Asn Ile Asp Tyr Gly Tyr Arg Phe		
	180	185 190
Ala Lys Glu Phe Val Asp Ala Arg Glu Arg Glu Arg Ile His Ala Lys		
	195	200 205
Gly Ser Tyr Glu Ser Ala Arg Ile Leu Met Asn Leu His Asn Asn Glu		
	210	215 220
Ala Gly Arg Arg Thr Val Tyr Asn Leu Ala Asp Val Ala Cys Lys Cys		
	225	230 235 240
His Gly Val Ala Gly Ser Cys Ser Leu Lys Thr Cys Trp Leu Gln Leu		
	245	250 255
Ala Asp Phe Arg Lys Val Gly Asp Ala Leu Lys Glu Lys Tyr Asp Ser		
	260	265 270
Ala Ala Ala Met Arg Leu Asn Ser Arg Gly Lys Leu Val Gln Val Asn		

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275	280	285
Ser Arg Phe Asn Ser Pro Thr Thr Gln Asp Leu Val Tyr Ile Asp Pro		
290	295	300
Ser Pro Asp Tyr Cys Val Arg Asn Glu Ser Thr Gly Ser Leu Gly Thr		
305	310	315
Gln Gly Arg Leu Cys Asn Lys Thr Ser Glu Gly Met Asp Gly Cys Glu		
	325	330
Leu Met Cys Cys Gly Arg Gly Tyr Asp Gln Phe Lys Thr Val Gln Thr		
	340	345
Glu Arg Cys His Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys Lys		
	355	360
Lys Cys Thr Glu Ile Val Asp Gln Phe Val Cys Lys		
	370	375
<210> SEQ ID NO 19		
<211> LENGTH: 380		
<212> TYPE: PRT		
<213> ORGANISM: Mus musculus		
<400> SEQUENCE: 19		
Met Lys Lys Pro Ile Gly Ile Leu Ser Pro Gly Val Ala Leu Gly Thr		
1	5	10
Ala Gly Gly Ala Met Ser Ser Lys Phe Phe Leu Met Ala Leu Ala Thr		
	20	25
Phe Phe Ser Phe Ala Gln Val Val Ile Glu Ala Asn Ser Trp Trp Ser		
	35	40
Leu Gly Met Asn Asn Pro Val Gln Met Ser Glu Val Tyr Ile Ile Gly		
	50	55
Ala Gln Pro Leu Cys Ser Gln Leu Ala Gly Leu Ser Gln Gly Gln Lys		
	65	70
Lys Leu Cys His Leu Tyr Gln Asp His Met Gln Tyr Ile Gly Glu Gly		
	85	90
Ala Lys Thr Gly Ile Lys Glu Cys Gln Tyr Gln Phe Arg His Arg Arg		
	100	105
Trp Asn Cys Ser Thr Val Asp Asn Thr Ser Val Phe Gly Arg Val Met		
	115	120
Gln Ile Gly Ser Arg Glu Thr Ala Phe Thr Tyr Ala Val Ser Ala Ala		
	130	135
Gly Val Val Asn Ala Met Ser Arg Ala Cys Arg Glu Gly Glu Leu Ser		
	145	150
Thr Cys Gly Cys Ser Arg Ala Ala Arg Pro Lys Asp Leu Pro Arg Asp		
	165	170
Trp Leu Trp Gly Gly Cys Gly Asp Asn Ile Asp Tyr Gly Tyr Arg Phe		
	180	185
Ala Lys Glu Phe Val Asp Ala Arg Glu Arg Glu Arg Ile His Ala Lys		
	195	200
Gly Ser Tyr Glu Ser Ala Arg Ile Leu Met Asn Leu His Asn Asn Glu		
	210	215
Ala Gly Arg Arg Thr Val Tyr Asn Leu Ala Asp Val Ala Cys Lys Cys		
	225	230
His Gly Val Ser Gly Ser Cys Ser Leu Lys Thr Cys Trp Leu Gln Leu		
	245	250
Ala Asp Phe Arg Lys Val Gly Asp Ala Leu Lys Glu Lys Tyr Asp Ser		
	260	265
		270

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Ala	Ala	Ala	Met	Arg	Leu	Asn	Ser	Arg	Gly	Lys	Leu	Val	Gln	Val	Asn
		275					280					285			
Ser	Arg	Phe	Asn	Ser	Pro	Thr	Thr	Gln	Asp	Leu	Val	Tyr	Ile	Asp	Pro
	290					295					300				
Ser	Pro	Asp	Tyr	Cys	Val	Arg	Asn	Glu	Ser	Thr	Gly	Ser	Leu	Gly	Thr
305					310					315					320
Gln	Gly	Arg	Leu	Cys	Asn	Lys	Thr	Ser	Glu	Gly	Met	Asp	Gly	Cys	Glu
			325						330					335	
Leu	Met	Cys	Cys	Gly	Arg	Gly	Tyr	Asp	Gln	Phe	Lys	Thr	Val	Gln	Thr
			340					345					350		
Glu	Arg	Cys	His	Cys	Lys	Phe	His	Trp	Cys	Cys	Tyr	Val	Lys	Cys	Lys
		355					360					365			
Lys	Cys	Thr	Glu	Ile	Val	Asp	Gln	Phe	Val	Cys	Lys				
	370					375					380				

<210> SEQ ID NO 20

<211> LENGTH: 379

<212> TYPE: PRT

<213> ORGANISM: Rattus norvegicus

<400> SEQUENCE: 20

Met	Lys	Lys	Pro	Ile	Gly	Ile	Leu	Ser	Pro	Gly	Val	Ala	Leu	Gly	Thr
1				5					10					15	
Ala	Gly	Gly	Ala	Met	Ser	Ser	Lys	Phe	Phe	Leu	Met	Ala	Leu	Ala	Thr
			20					25					30		
Phe	Phe	Ser	Phe	Ala	Gln	Val	Val	Ile	Lys	Ala	Asn	Ser	Trp	Trp	Ser
		35				40					45				
Leu	Ser	Met	Asn	Asn	Pro	Val	Gln	Met	Ser	Glu	Val	Tyr	Ile	Ile	Gly
	50					55					60				
Ala	Gln	Pro	Leu	Cys	Ser	Gln	Leu	Ala	Gly	Leu	Ser	Gln	Gly	Gln	Lys
65					70					75					80
Lys	Leu	Cys	His	Leu	Tyr	Gln	Asp	His	Met	Gln	Tyr	Ile	Gly	Glu	Gly
			85						90					95	
Ala	Lys	Thr	Gly	Ile	Lys	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	His	Arg	Arg
			100					105					110		
Trp	Asn	Cys	Ser	Thr	Val	Asp	Asn	Thr	Ser	Val	Phe	Gly	Arg	Val	Met
	115						120					125			
Gln	Ile	Gly	Ser	Arg	Glu	Thr	Ala	Phe	Thr	Tyr	Ala	Val	Ser	Ala	Ala
	130					135					140				
Gly	Val	Val	Asn	Ala	Met	Ser	Arg	Ala	Cys	Arg	Glu	Gly	Glu	Leu	Ser
145					150					155					160
Thr	Cys	Gly	Cys	Ser	Arg	Ala	Arg	Pro	Lys	Asp	Leu	Pro	Arg	Asp	Trp
				165					170					175	
Leu	Trp	Gly	Gly	Cys	Gly	Asp	Asn	Ile	Asp	Tyr	Gly	Tyr	Arg	Phe	Ala
		180					185						190		
Lys	Glu	Phe	Val	Asp	Ala	Arg	Glu	Arg	Glu	Arg	Ile	His	Ala	Lys	Gly
		195					200					205			
Ser	Tyr	Glu	Ser	Ala	Arg	Ile	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala
	210					215					220				
Gly	Arg	Arg	Thr	Val	Tyr	Asn	Leu	Ala	Asp	Val	Ala	Cys	Lys	Cys	His
225						230				235					240
Gly	Val	Ser	Gly	Ser	Cys	Ser	Leu	Lys	Thr	Cys	Trp	Leu	Gln	Leu	Ala
				245					250					255	
Asp	Phe	Arg	Lys	Val	Gly	Asp	Ala	Leu	Lys	Glu	Lys	Tyr	Asp	Ser	Ala
			260					265					270		

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Ala Ala Met Arg Leu Asn Ser Arg Gly Lys Leu Val Gln Val Asn Ser
 275 280 285

Arg Phe Asn Ser Pro Thr Thr Gln Asp Leu Val Tyr Ile Asp Pro Ser
 290 295 300

Pro Asp Tyr Cys Val Arg Asn Glu Ser Thr Gly Ser Leu Gly Thr Gln
 305 310 315 320

Gly Arg Leu Cys Asn Lys Thr Ser Glu Gly Met Asp Gly Cys Glu Leu
 325 330 335

Met Cys Cys Gly Arg Gly Tyr Asp Gln Phe Lys Thr Val Gln Thr Glu
 340 345 350

Arg Cys His Cys Lys Phe His Trp Cys Cys Tyr Val Lys Cys Lys Lys
 355 360 365

Cys Thr Glu Ile Val Asp Gln Phe Val Cys Lys
 370 375

<210> SEQ ID NO 21

<211> LENGTH: 385

<212> TYPE: PRT

<213> ORGANISM: Gallus gallus

<400> SEQUENCE: 21

Met Glu Lys Ser Thr Ala Val Leu Ile Gln Gly Gly Ala Leu Gly Thr
 1 5 10 15

Leu Gly Ser Thr Met Ala Ser Gln Tyr Leu Val Val Ala Leu Ala Ile
 20 25 30

Phe Ser Ser Cys Thr Gln Val Val Ile Glu Ala Ser Ser Trp Trp Ser
 35 40 45

Leu Gly Met Asn Pro Met Asn Pro Met Asn Pro Val Gln Met Ser Glu
 50 55 60

Val Tyr Ile Ile Gly Ala Gln Pro Leu Cys Ser Gln Leu Ala Gly Leu
 65 70 75 80

Ser Gln Gly Gln Lys Lys Leu Cys Gln Leu Tyr Gln Asp His Met Gln
 85 90 95

Phe Ile Gly Glu Gly Ala Lys Thr Gly Ile Lys Glu Cys Gln Tyr Gln
 100 105 110

Phe Arg His Arg Arg Trp Asn Cys Ser Thr Val Asp Asn Asn Ser Val
 115 120 125

Phe Gly Arg Val Met Gln Ile Gly Ser Arg Glu Thr Ala Phe Thr Tyr
 130 135 140

Ala Val Ser Ala Ala Gly Val Val Asn Ala Met Ser Arg Ala Cys Arg
 145 150 155 160

Glu Gly Glu Leu Ser Ser Cys Gly Cys Ser Arg Ala Ala Arg Pro Lys
 165 170 175

Asp Leu Pro Arg Asp Trp Leu Trp Gly Gly Cys Gly Asp Asn Ile Glu
 180 185 190

Tyr Gly Tyr Arg Phe Ala Lys Glu Phe Val Asp Ala Arg Glu Arg Glu
 195 200 205

Arg Val Tyr Gln Arg Gly Ser Tyr Glu Ser Ala Arg Ile Met Met Asn
 210 215 220

Leu His Asn Asn Glu Ala Gly Arg Arg Thr Val Tyr Asn Leu Ala Asp
 225 230 235 240

Val Ala Cys Lys Cys His Gly Val Ser Gly Ser Cys Ser Leu Lys Thr
 245 250 255

Cys Trp Leu Gln Leu Ala Asp Phe Arg Lys Val Gly Asp Ala Leu Lys

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260	265	270
Glu Lys Tyr Asp Ser Ala Ala Ala Met Lys Leu Asn Ser Arg Gly Lys		
275	280	285
Leu Val Gln Met Asn Ser Arg Phe Asn Ala Pro Thr Ile His Asp Leu		
290	295	300
Ile Tyr Ile Asp Pro Ser Pro Asp Tyr Cys Met Arg Asn Glu Ser Thr		
305	310	315
Gly Ser Leu Gly Thr Gln Gly Arg Leu Cys Asn Lys Thr Ser Glu Gly		
325	330	335
Met Asp Gly Cys Glu Leu Met Cys Cys Gly Arg Gly Tyr Asp Gln Phe		
340	345	350
Lys Thr Val Gln Arg Glu Arg Cys His Cys Lys Phe His Trp Cys Cys		
355	360	365
Tyr Val Lys Cys Lys Leu Cys Thr Glu Ile Val Asp Gln Phe Val Cys		
370	375	380
Lys		
385		
 <210> SEQ ID NO 22		
<211> LENGTH: 374		
<212> TYPE: PRT		
<213> ORGANISM: Danio rerio		
 <400> SEQUENCE: 22		
Met Met Leu Leu Lys Leu Lys Trp Thr Ser Ser Gly Val Lys Asp Thr		
1	5	10
Pro His Thr Leu Leu Ser Ile Ile Ile Thr Phe Cys Val Phe Phe Met		
20	25	30
Leu Glu Ile Val Asp Ala Asn Ser Trp Trp Ser Leu Ala Met Asn Pro		
35	40	45
Leu Leu Ile Pro Glu Val Tyr Val Ile Gly Gly Gln Pro Leu Cys Ser		
50	55	60
Gln Leu Ser Gly Leu Ser Lys Gly Gln Lys Lys Leu Cys Gln Leu Tyr		
65	70	75
Gln Asp His Met Gln Tyr Ile Gly Glu Gly Ala Lys Thr Gly Ile Arg		
85	90	95
Glu Cys Gln His Gln Phe Arg His Arg Arg Trp Asn Cys Ser Thr Val		
100	105	110
Asp Asn Ser Thr Val Leu Gly Arg Val Met His Ile Gly Ser Arg Glu		
115	120	125
Ser Ala Phe Ala Phe Ala Ile Ser Ala Ala Gly Val Leu His Ala Val		
130	135	140
Ser Arg Ala Cys Arg Glu Gly Ala Leu Ser Ser Cys Gly Cys Ser Arg		
145	150	155
Ala Ser Arg Pro Lys Asp Leu Pro Arg Asp Trp Leu Trp Gly Gly Cys		
165	170	175
Gly Asp Asn Leu Asn Tyr Gly Tyr Arg Phe Ser Arg Glu Phe Val Asp		
180	185	190
Ala Arg Glu Arg Glu Lys Thr Phe Ser Lys Gly Ser Ala Glu Ser Ala		
195	200	205
Arg Gln Met Met Asn Leu His Asn Asn Glu Ala Gly Arg Arg Ile Val		
210	215	220
Ser Asp Leu Ala Asp Val Ser Cys Lys Cys His Gly Val Ser Gly Ser		
225	230	235
		240

Cys	Ser	Leu	Lys	Thr	Cys	Trp	Leu	Gln	Leu	Ala	Asp	Phe	Arg	Lys	Val		
				245					250				255				
Gly	Asp	Val	Leu	Lys	Glu	Lys	Tyr	Asp	Ser	Ala	Ala	Ala	Met	Arg	Met		
				260					265					270			
Asn	Gly	Arg	Gly	Lys	Leu	Val	Gln	Met	His	Ser	Lys	Phe	Ser	Pro	Pro		
				275					280					285			
Ser	Gly	Gln	Asp	Leu	Leu	Tyr	Leu	Gln	Pro	Ser	Pro	Asp	Tyr	Cys	Ile		
				290					295					300			
Arg	Asn	Ser	Ser	Ser	Gly	Ser	Leu	Gly	Thr	Gln	Gly	Arg	Leu	Cys	Asn		
305								310					315			320	
Lys	Thr	Ser	Glu	Gly	Met	Asp	Gly	Cys	Ala	Leu	Met	Cys	Cys	Gly	Arg		
				325								330				335	
Gly	Tyr	Asp	Gln	Tyr	Lys	Ala	Glu	Leu	Val	Glu	Arg	Cys	His	Cys	Lys		
				340								345				350	
Phe	His	Trp	Cys	Cys	Tyr	Val	Arg	Cys	Lys	Arg	Cys	Ser	Ser	Ile	Val		
				355								360				365	
Asp	Gln	Tyr	Val	Cys	Lys												
370																	

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<210> SEQ ID NO 23
<211> LENGTH: 380
<212> TYPE: PRT
<213> ORGANISM: Bos taurus

<400> SEQUENCE: 23
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Met 1	Lys	Lys	Ser	Ile 5	Gly	Ile	Leu	Ser	Pro 10	Gly	Val	Ala	Trp	Gly 15	Thr
Ala	Gly	Arg	Ala 20	Met	Ser	Ser	Lys	Phe 25	Phe	Leu	Met	Ala	Leu 30	Ala	Ile
Phe	Leu	Ser 35	Phe	Ala	Gln	Val 40	Val	Ile	Glu	Ala	Asn 45	Ser	Trp	Trp	Ser
Leu 50	Gly	Met	Asn	Asn	Pro 55	Val	Gln	Met	Ser	Glu	Val 60	Tyr	Ile	Ile	Gly
Ala 65	Gln	Pro	Leu	Cys 70	Ser	Gln	Leu	Ala	Gly	Leu 75	Ser	Gln	Gly	Gln	Lys 80
Lys	Leu	Cys	His 85	Leu	Tyr	Gln	Asp	His 90	Met	Gln	Tyr	Ile	Gly	Glu 95	Gly
Ala	Lys	Thr	Gly 100	Ile	Lys	Glu	Cys	Gln 105	Tyr	Gln	Phe	Arg 110	His	Arg	Arg
Trp	Asn	Cys 115	Ser	Thr	Val	Asp 120	Asn	Thr	Ser	Val	Phe	Gly 125	Arg	Val	Met
Gln 130	Ile	Gly	Ser	Arg	Glu 135	Thr	Ala	Phe	Thr	Tyr	Ala 140	Val	Ser	Ala	Ala
Gly 145	Val	Val	Asn	Ala 150	Met	Ser	Arg	Ala	Cys	Arg 155	Glu	Gly	Glu	Leu	Ser 160
Thr	Cys	Gly	Cys 165	Ser	Arg	Ala	Ala	Arg 170	Pro	Lys	Asp	Leu	Pro	Arg 175	Asp
Trp	Leu	Trp	Gly 180	Gly	Cys	Gly	Asp 185	Asn	Ile	Asp	Tyr	Gly 190	Tyr	Arg	Phe
Ala	Lys	Glu 195	Phe	Val	Asp 200	Ala	Arg	Glu	Arg	Glu	Arg 205	Ile	His	Ala	Lys
Gly 210	Ser	Tyr	Glu	Ser	Ala 215	Arg	Ile	Leu	Met	Asn 220	Leu	His	Asn	Asn	Glu
Ala 225	Gly	Arg	Arg	Thr 230	Val	Tyr	Ser	Leu	Ala 235	Asp	Val	Ala	Cys	Lys	Cys 240

His	Gly	Val	Ser	Gly	Ser	Cys	Ser	Leu	Lys	Thr	Cys	Trp	Leu	Gln	Leu	
				245					250					255		
Ala	Asp	Phe	Arg	Lys	Val	Gly	Asp	Ala	Leu	Lys	Glu	Lys	Tyr	Asp	Ser	
			260					265					270			
Ala	Ala	Ala	Met	Arg	Leu	Asn	Ser	Arg	Gly	Lys	Leu	Val	Gln	Val	Asn	
		275					280					285				
Ser	Arg	Phe	Asn	Ser	Pro	Thr	Thr	Gln	Asp	Leu	Val	Tyr	Ile	Asp	Pro	
	290					295					300					
Ser	Pro	Asp	Tyr	Cys	Val	Arg	Asn	Glu	Ser	Thr	Gly	Ser	Leu	Gly	Thr	
305					310					315					320	
Gln	Gly	Arg	Leu	Cys	Asn	Lys	Thr	Ser	Glu	Gly	Met	Asp	Gly	Cys	Glu	
				325					330					335		
Leu	Met	Cys	Cys	Gly	Arg	Gly	Tyr	Asp	Gln	Phe	Lys	Thr	Val	Gln	Thr	
			340					345					350			
Glu	Arg	Cys	His	Cys	Lys	Phe	His	Trp	Cys	Cys	Tyr	Val	Lys	Cys	Lys	
		355					360					365				
Lys	Cys	Thr	Glu	Ile	Val	Asp	Gln	Phe	Val	Cys	Lys					
	370					375					380					

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<210> SEQ ID NO 24
<211> LENGTH: 370
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
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<400> SEQUENCE: 24

Met 1	Gly	Leu	Trp	Ala 5	Leu	Leu	Pro	Gly	Trp 10	Val	Ser	Ala	Thr	Leu 15	Leu
Leu	Ala	Leu	Ala 20	Ala	Leu	Pro	Ala	Ala 25	Leu	Ala	Ala	Asn 30	Ser	Ser	Gly
Arg	Trp	Trp	Gly 35	Ile	Val	Asn	Val 40	Ala	Ser	Ser	Thr	Asn 45	Leu	Leu	Thr
Asp	Ser	Lys	Ser	Leu	Gln	Leu 55	Val	Leu	Glu	Pro	Ser 60	Leu	Gln	Leu	Leu
Ser 65	Arg	Lys	Gln	Arg	Arg 70	Leu	Ile	Arg	Gln	Asn 75	Pro	Gly	Ile	Leu	His 80
Ser	Val	Ser	Gly 85	Gly	Leu	Gln	Ser	Ala	Val 90	Arg	Glu	Cys	Lys	Trp 95	Gln
Phe	Arg	Asn	Arg 100	Arg	Trp	Asn	Cys	Pro 105	Thr	Ala	Pro	Gly	Pro 110	His	Leu
Phe	Gly	Lys 115	Ile	Val	Asn	Arg	Gly 120	Cys	Arg	Glu	Thr	Ala 125	Phe	Ile	Phe
Ala	Ile 130	Thr	Ser	Ala	Gly	Val 135	Thr	His	Ser	Val	Ala 140	Arg	Ser	Cys	Ser
Glu 145	Gly	Ser	Ile	Glu	Ser 150	Cys	Thr	Cys	Asp 155	Tyr	Arg	Arg	Arg	Gly	Pro 160
Gly	Gly	Pro	Asp 165	Trp	His	Trp	Gly	Gly	Cys 170	Ser	Asp	Asn	Ile	Asp 175	Phe
Gly	Arg	Leu	Phe 180	Gly	Arg	Glu	Phe	Val 185	Asp	Ser	Gly	Glu	Lys 190	Gly	Arg
Asp	Leu 195	Arg	Phe	Leu	Met	Asn	Leu 200	His	Asn	Asn	Glu	Ala 205	Gly	Arg	Thr
Thr 210	Val	Phe	Ser	Glu	Met	Arg 215	Gln	Glu	Cys	Lys	Cys 220	His	Gly	Met	Ser
Gly	Ser	Cys	Thr	Val	Arg	Thr	Cys	Trp	Met	Arg	Leu	Pro	Thr	Leu	Arg

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225	230	235	240
Ala Val Gly Asp	Val Leu Arg Asp Arg Phe Asp Gly Ala Ser Arg Val		
	245	250	255
Leu Tyr Gly Asn Arg Gly Ser Asn Arg Ala Ser Arg Ala Glu Leu Leu			
	260	265	270
Arg Leu Glu Pro Glu Asp Pro Ala His Lys Pro Pro Ser Pro His Asp			
	275	280	285
Leu Val Tyr Phe Glu Lys Ser Pro Asn Phe Cys Thr Tyr Ser Gly Arg			
	290	295	300
Leu Gly Thr Ala Gly Thr Ala Gly Arg Ala Cys Asn Ser Ser Ser Pro			
	305	310	315
Ala Leu Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly His Arg Thr			
	325	330	335
Arg Thr Gln Arg Val Thr Glu Arg Cys Asn Cys Thr Phe His Trp Cys			
	340	345	350
Cys His Val Ser Cys Arg Asn Cys Thr His Thr Arg Val Leu His Glu			
	355	360	365
Cys Leu			
	370		

<210> SEQ ID NO 25

<211> LENGTH: 360

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

Met Asn Ala Pro	Leu Gly Gly Ile Trp	Leu Trp Leu Pro	Leu Leu Leu
1	5	10	15
Thr Trp Leu Thr	Pro Glu Val Asn Ser Ser Trp Trp Tyr Met Arg Ala		
	20	25	30
Thr Gly Gly Ser Ser Arg Val Met Cys Asp Asn Val Pro Gly Leu Val			
	35	40	45
Ser Ser Gln Arg Gln Leu Cys His Arg His Pro Asp Val Met Arg Ala			
	50	55	60
Ile Ser Gln Gly Val Ala Glu Trp Thr Ala Glu Cys Gln His Gln Phe			
	65	70	75
Arg Gln His Arg Trp Asn Cys Asn Thr Leu Asp Arg Asp His Ser Leu			
	85	90	95
Phe Gly Arg Val Leu Leu Arg Ser Ser Arg Glu Ser Ala Phe Val Tyr			
	100	105	110
Ala Ile Ser Ser Ala Gly Val Val Phe Ala Ile Thr Arg Ala Cys Ser			
	115	120	125
Gln Gly Glu Val Lys Ser Cys Ser Cys Asp Pro Lys Lys Met Gly Ser			
	130	135	140
Ala Lys Asp Ser Lys Gly Ile Phe Asp Trp Gly Gly Cys Ser Asp Asn			
	145	150	155
Ile Asp Tyr Gly Ile Lys Phe Ala Arg Ala Phe Val Asp Ala Lys Glu			
	165	170	175
Arg Lys Gly Lys Asp Ala Arg Ala Leu Met Asn Leu His Asn Asn Arg			
	180	185	190
Ala Gly Arg Lys Ala Val Lys Arg Phe Leu Lys Gln Glu Cys Lys Cys			
	195	200	205
His Gly Val Ser Gly Ser Cys Thr Leu Arg Thr Cys Trp Leu Ala Met			
	210	215	220

-continued

Ala Asp Phe Arg Lys Thr Gly Asp Tyr Leu Trp Arg Lys Tyr Asn Gly
 225 230 235 240
 Ala Ile Gln Val Val Met Asn Gln Asp Gly Thr Gly Phe Thr Val Ala
 245 250 255
 Asn Glu Arg Phe Lys Lys Pro Thr Lys Asn Asp Leu Val Tyr Phe Glu
 260 265 270
 Asn Ser Pro Asp Tyr Cys Ile Arg Asp Arg Glu Ala Gly Ser Leu Gly
 275 280 285
 Thr Ala Gly Arg Val Cys Asn Leu Thr Ser Arg Gly Met Asp Ser Cys
 290 295 300
 Glu Val Met Cys Cys Gly Arg Gly Tyr Asp Thr Ser His Val Thr Arg
 305 310 315 320
 Met Thr Lys Cys Gly Cys Lys Phe His Trp Cys Cys Ala Val Arg Cys
 325 330 335
 Gln Asp Cys Leu Glu Ala Leu Asp Val His Thr Cys Lys Ala Pro Lys
 340 345 350
 Asn Ala Asp Trp Thr Thr Ala Thr
 355 360

 <210> SEQ ID NO 26
 <211> LENGTH: 372
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

 <400> SEQUENCE: 26

 Met Leu Asp Gly Leu Gly Val Val Ala Ile Ser Ile Phe Gly Ile Gln
 1 5 10 15
 Leu Lys Thr Glu Gly Ser Leu Arg Thr Ala Val Pro Gly Ile Pro Thr
 20 25 30
 Gln Ser Ala Phe Asn Lys Cys Leu Gln Arg Tyr Ile Gly Ala Leu Gly
 35 40 45
 Ala Arg Val Ile Cys Asp Asn Ile Pro Gly Leu Val Ser Arg Gln Arg
 50 55 60
 Gln Leu Cys Gln Arg Tyr Pro Asp Ile Met Arg Ser Val Gly Glu Gly
 65 70 75 80
 Ala Arg Glu Trp Ile Arg Glu Cys Gln His Gln Phe Arg His His Arg
 85 90 95
 Trp Asn Cys Thr Thr Leu Asp Arg Asp His Thr Val Phe Gly Arg Val
 100 105 110
 Met Leu Arg Ser Ser Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser
 115 120 125
 Ala Gly Val Val His Ala Ile Thr Arg Ala Cys Ser Gln Gly Glu Leu
 130 135 140
 Ser Val Cys Ser Cys Asp Pro Tyr Thr Arg Gly Arg His His Asp Gln
 145 150 155 160
 Arg Gly Asp Phe Asp Trp Gly Gly Cys Ser Asp Asn Ile His Tyr Gly
 165 170 175
 Val Arg Phe Ala Lys Ala Phe Val Asp Ala Lys Glu Lys Arg Leu Lys
 180 185 190
 Asp Ala Arg Ala Leu Met Asn Leu His Asn Asn Arg Cys Gly Arg Thr
 195 200 205
 Ala Val Arg Arg Phe Leu Lys Leu Glu Cys Lys Cys His Gly Val Ser
 210 215 220
 Gly Ser Cys Thr Leu Arg Thr Cys Trp Arg Ala Leu Ser Asp Phe Arg
 225 230 235 240

Met 1	Glu	Pro	His	Leu 5	Leu	Gly	Leu	Leu	Leu 10	Gly	Leu	Leu	Leu	Gly 15	Gly
Thr	Arg	Val	Leu 20	Ala	Gly	Tyr	Pro	Ile 25	Trp	Trp	Ser	Leu	Ala 30	Leu	Gly
Gln	Gln	Tyr 35	Thr	Ser	Leu	Gly	Ser 40	Gln	Pro	Leu	Leu	Cys 45	Gly	Ser	Ile
Pro	Gly 50	Leu	Val	Pro	Lys	Gln 55	Leu	Arg	Phe	Cys 60	Arg	Asn	Tyr	Ile	Glu
Ile 65	Met	Pro	Ser	Val	Ala 70	Glu	Gly	Val	Lys	Leu 75	Gly	Ile	Gln	Glu	Cys 80
Gln	His	Gln	Phe 85	Arg	Gly	Arg	Arg	Trp	Asn 90	Cys	Thr	Thr	Ile	Asp 95	Asp
Ser	Leu	Ala	Ile 100	Phe	Gly	Pro	Val	Leu 105	Asp	Lys	Ala	Thr	Arg 110	Glu	Ser
Ala	Phe 115	Val	His	Ala	Ile	Ala	Ser 120	Ala	Gly	Val	Ala	Phe 125	Ala	Val	Thr
Arg	Ser 130	Cys	Ala	Glu	Gly	Thr 135	Ser	Thr	Ile	Cys	Gly 140	Cys	Asp	Ser	His
His 145	Lys	Gly	Pro	Pro	Gly 150	Glu	Gly	Trp	Lys	Trp 155	Gly	Gly	Cys	Ser	Glu 160
Asp	Ala	Asp	Phe 165	Gly	Val	Leu	Val	Ser	Arg 170	Glu	Phe	Ala	Asp 175	Ala	Arg
Glu	Asn	Arg	Pro 180	Asp	Ala	Arg	Ser	Ala 185	Met	Asn	Lys	His	Asn 190	Asn	Glu
Ala	Gly 195	Arg	Thr	Thr	Ile	Leu	Asp 200	His	Met	His	Leu	Lys 205	Cys	Lys	Cys
His 210	Gly	Leu	Ser	Gly	Ser	Cys 215	Glu	Val	Lys	Thr	Cys 220	Trp	Trp	Ala	Gln
Pro	Asp	Phe	Arg	Ala	Ile	Gly	Asp	Phe	Leu	Lys	Asp	Lys	Tyr	Asp	Ser

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225	230	235	240
Ala Ser Glu Met Val Val Glu Lys His Arg Glu Ser Arg Gly Trp Val	245	250	255
Glu Thr Leu Arg Ala Lys Tyr Ser Leu Phe Lys Pro Pro Thr Glu Arg	260	265	270
Asp Leu Val Tyr Tyr Glu Asn Ser Pro Asn Phe Cys Glu Pro Asn Pro	275	280	285
Glu Thr Gly Ser Phe Gly Thr Arg Asp Arg Thr Cys Asn Val Thr Ser	290	295	300
His Gly Ile Asp Gly Cys Asp Leu Leu Cys Cys Gly Arg Gly His Asn	305	310	315
Thr Arg Thr Glu Lys Arg Lys Glu Lys Cys His Cys Ile Phe His Trp	325	330	335
Cys Cys Tyr Val Ser Cys Gln Glu Cys Ile Arg Ile Tyr Asp Val His	340	345	350
Thr Cys Lys	355		

<210> SEQ ID NO 28
 <211> LENGTH: 352
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 28

Met Ala Pro Leu Gly Tyr Phe Leu Leu Leu Cys Ser Leu Lys Gln Ala	1	5	10	15
Leu Gly Ser Tyr Pro Ile Trp Trp Ser Leu Ala Val Gly Pro Gln Tyr	20	25	30	
Ser Ser Leu Gly Ser Gln Pro Ile Leu Cys Ala Ser Ile Pro Gly Leu	35	40	45	
Val Pro Lys Gln Leu Arg Phe Cys Arg Asn Tyr Val Glu Ile Met Pro	50	55	60	
Ser Val Ala Glu Gly Ile Lys Ile Gly Ile Gln Glu Cys Gln His Gln	65	70	75	80
Phe Arg Gly Arg Arg Trp Asn Cys Thr Thr Val His Asp Ser Leu Ala	85	90	95	
Ile Phe Gly Pro Val Leu Asp Lys Ala Thr Arg Glu Ser Ala Phe Val	100	105	110	
His Ala Ile Ala Ser Ala Gly Val Ala Phe Ala Val Thr Arg Ser Cys	115	120	125	
Ala Glu Gly Thr Ala Ala Ile Cys Gly Cys Ser Ser Arg His Gln Gly	130	135	140	
Ser Pro Gly Lys Gly Trp Lys Trp Gly Gly Cys Ser Glu Asp Ile Glu	145	150	155	160
Phe Gly Gly Met Val Ser Arg Glu Phe Ala Asp Ala Arg Glu Asn Arg	165	170	175	
Pro Asp Ala Arg Ser Ala Met Asn Arg His Asn Asn Glu Ala Gly Arg	180	185	190	
Gln Ala Ile Ala Ser His Met His Leu Lys Cys Lys Cys His Gly Leu	195	200	205	
Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Trp Ser Gln Pro Asp Phe	210	215	220	
Arg Ala Ile Gly Asp Phe Leu Lys Asp Lys Tyr Asp Ser Ala Ser Glu	225	230	235	240

-continued

Met	Val	Val	Glu	Lys	His	Arg	Glu	Ser	Arg	Gly	Trp	Val	Glu	Thr	Leu
				245						250				255	
Arg	Pro	Arg	Tyr	Thr	Tyr	Phe	Lys	Val	Pro	Thr	Glu	Arg	Asp	Leu	Val
			260					265					270		
Tyr	Tyr	Glu	Ala	Ser	Pro	Asn	Phe	Cys	Glu	Pro	Asn	Pro	Glu	Thr	Gly
		275					280					285			
Ser	Phe	Gly	Thr	Arg	Asp	Arg	Thr	Cys	Asn	Val	Ser	Ser	His	Gly	Ile
	290					295					300				
Asp	Gly	Cys	Asp	Leu	Leu	Cys	Cys	Gly	Arg	Gly	His	Asn	Ala	Arg	Ala
305					310					315					320
Glu	Arg	Arg	Arg	Glu	Lys	Cys	Arg	Cys	Val	Phe	His	Trp	Cys	Cys	Tyr
				325					330					335	
Val	Ser	Cys	Gln	Glu	Cys	Thr	Arg	Val	Tyr	Asp	Val	His	Thr	Cys	Lys
			340					345					350		

<210> SEQ ID NO 29

<211> LENGTH: 351

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe	Ala
1				5					10					15	
Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys	Leu	Ser
		20					25						30		
Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys	Leu	Lys	Gly
		35				40						45			
Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn	Leu	Glu	Val	Met
	50				55						60				
Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile	Glu	Glu	Cys	Gln	Tyr
65				70					75					80	
Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser	Thr	Leu	Asp	Ser	Leu	Pro
			85					90						95	
Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly	Thr	Arg	Glu	Ala	Ala	Phe	Val
		100					105						110		
Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val	Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys
	115					120						125			
Ser	Ser	Gly	Glu	Leu	Glu	Lys	Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly
	130					135					140				
Val	Ser	Pro	Gln	Gly	Phe	Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala
145				150					155					160	
Tyr	Gly	Val	Ala	Phe	Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser
			165					170						175	
Lys	Gly	Ala	Ser	Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu
		180					185						190		
Ala	Gly	Arg	Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys
		195				200						205			
His	Gly	Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val
	210					215					220				
Pro	Pro	Phe	Arg	Gln	Val	Gly	His	Ala	Leu	Lys	Glu	Lys	Phe	Asp	Gly
225					230					235				240	
Ala	Thr	Glu	Val	Glu	Pro	Arg	Arg	Val	Gly	Ser	Ser	Arg	Ala	Leu	Val
			245					250						255	
Pro	Arg	Asn	Ala	Gln	Phe	Lys	Pro	His	Thr	Asp	Glu	Asp	Leu	Val	Tyr
		260					265						270		

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Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg Ser Gly Val
 275 280 285

Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser Lys Ala Ile Asp
 290 295 300

Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe His Thr Ala Gln Val
 305 310 315 320

Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe His Trp Cys Cys Phe Val
 325 330 335

Lys Cys Arg Gln Cys Gln Arg Leu Val Glu Leu His Thr Cys Arg
 340 345 350

<210> SEQ ID NO 30
 <211> LENGTH: 359
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 30

Met Pro Ser Leu Leu Leu Leu Phe Thr Ala Ala Leu Leu Ser Ser Trp
 1 5 10 15

Ala Gln Leu Leu Thr Asp Ala Asn Ser Trp Trp Ser Leu Ala Leu Asn
 20 25 30

Pro Val Gln Arg Pro Glu Met Phe Ile Ile Gly Ala Gln Pro Val Cys
 35 40 45

Ser Gln Leu Pro Gly Leu Ser Pro Gly Gln Arg Lys Leu Cys Gln Leu
 50 55 60

Tyr Gln Glu His Met Ala Tyr Ile Gly Glu Gly Ala Lys Thr Gly Ile
 65 70 75 80

Lys Glu Cys Gln His Gln Phe Arg Gln Arg Arg Trp Asn Cys Ser Thr
 85 90 95

Ala Asp Asn Ala Ser Val Phe Gly Arg Val Met Gln Ile Gly Ser Arg
 100 105 110

Glu Thr Ala Phe Thr His Ala Val Ser Ala Ala Gly Val Val Asn Ala
 115 120 125

Ile Ser Arg Ala Cys Arg Glu Gly Glu Leu Ser Thr Cys Gly Cys Ser
 130 135 140

Arg Thr Ala Arg Pro Lys Asp Leu Pro Arg Asp Trp Leu Trp Gly Gly
 145 150 155 160

Cys Gly Asp Asn Val Glu Tyr Gly Tyr Arg Phe Ala Lys Glu Phe Val
 165 170 175

Asp Ala Arg Glu Arg Glu Lys Asn Phe Ala Lys Gly Ser Glu Glu Gln
 180 185 190

Gly Arg Val Leu Met Asn Leu Gln Asn Asn Glu Ala Gly Arg Arg Ala
 195 200 205

Val Tyr Lys Met Ala Asp Val Ala Cys Lys Cys His Gly Val Ser Gly
 210 215 220

Ser Cys Ser Leu Lys Thr Cys Trp Leu Gln Leu Ala Glu Phe Arg Lys
 225 230 235 240

Val Gly Asp Arg Leu Lys Glu Lys Tyr Asp Ser Ala Ala Ala Met Arg
 245 250 255

Val Thr Arg Lys Gly Arg Leu Glu Leu Val Asn Ser Arg Phe Thr Gln
 260 265 270

Pro Thr Pro Glu Asp Leu Val Tyr Val Asp Pro Ser Pro Asp Tyr Cys
 275 280 285

Leu Arg Asn Glu Ser Thr Gly Ser Leu Gly Thr Gln Gly Arg Leu Cys

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290	295	300
Asn Lys Thr Ser Glu Gly Met Asp Gly Cys Glu Leu Met Cys Cys Gly		
305	310	315 320
Arg Gly Tyr Asn Gln Phe Lys Ser Val Gln Val Glu Arg Cys His Cys		
	325	330 335
Lys Phe His Trp Cys Cys Phe Val Arg Cys Lys Lys Cys Thr Glu Ile		
	340	345 350
Val Asp Gln Tyr Ile Cys Lys		
	355	
<210> SEQ ID NO 31		
<211> LENGTH: 365		
<212> TYPE: PRT		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 31		
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu		
1	5	10 15
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro		
	20	25 30
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala		
	35	40 45
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu		
	50	55 60
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe		
	65	70 75 80
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg		
	85	90 95
Ile Leu Gln Gln Asp Ile Arg Glu Thr Ala Phe Val Phe Ala Ile Thr		
	100	105 110
Ala Ala Gly Ala Ser His Ala Val Thr Gln Ala Cys Ser Met Gly Glu		
	115	120 125
Leu Leu Gln Cys Gly Cys Gln Ala Pro Arg Gly Arg Ala Pro Pro Arg		
	130	135 140
Pro Ser Gly Leu Pro Gly Thr Pro Gly Pro Pro Gly Pro Ala Gly Ser		
	145	150 155 160
Pro Glu Gly Ser Ala Ala Trp Glu Trp Gly Gly Cys Gly Asp Asp Val		
	165	170 175
Asp Phe Gly Asp Glu Lys Ser Arg Leu Phe Met Asp Ala Arg His Lys		
	180	185 190
Arg Gly Arg Gly Asp Ile Arg Ala Leu Val Gln Leu His Asn Asn Glu		
	195	200 205
Ala Gly Arg Leu Ala Val Arg Ser His Thr Arg Thr Glu Cys Lys Cys		
	210	215 220
His Gly Leu Ser Gly Ser Cys Ala Leu Arg Thr Cys Trp Gln Lys Leu		
	225	230 235 240
Pro Pro Phe Arg Glu Val Gly Ala Arg Leu Leu Glu Arg Phe His Gly		
	245	250 255
Ala Ser Arg Val Met Gly Thr Asn Asp Gly Lys Ala Leu Leu Pro Ala		
	260	265 270
Val Arg Thr Leu Lys Pro Pro Gly Arg Ala Asp Leu Leu Tyr Ala Ala		
	275	280 285
Asp Ser Pro Asp Phe Cys Ala Pro Asn Arg Arg Thr Gly Ser Pro Gly		
	290	295 300

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Thr Arg Gly Arg Ala Cys Asn Ser Ser Ala Pro Asp Leu Ser Gly Cys
 305 310 315 320

Asp Leu Leu Cys Cys Gly Arg Gly His Arg Gln Glu Ser Val Gln Leu
 325 330 335

Glu Glu Asn Cys Leu Cys Arg Phe His Trp Cys Cys Val Val Gln Cys
 340 345 350

His Arg Cys Arg Val Arg Lys Glu Leu Ser Leu Cys Leu
 355 360 365

<210> SEQ ID NO 32
 <211> LENGTH: 349
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 32

Met His Arg Asn Phe Arg Lys Trp Ile Phe Tyr Val Phe Leu Cys Phe
 1 5 10 15

Gly Val Leu Tyr Val Lys Leu Gly Ala Leu Ser Ser Val Val Ala Leu
 20 25 30

Gly Ala Asn Ile Ile Cys Asn Lys Ile Pro Gly Leu Ala Pro Arg Gln
 35 40 45

Arg Ala Ile Cys Gln Ser Arg Pro Asp Ala Ile Ile Val Ile Gly Glu
 50 55 60

Gly Ala Gln Met Gly Ile Asn Glu Cys Gln Tyr Gln Phe Arg Phe Gly
 65 70 75 80

Arg Trp Asn Cys Ser Ala Leu Gly Glu Lys Thr Val Phe Gly Gln Glu
 85 90 95

Leu Arg Val Gly Ser Arg Glu Ala Ala Phe Thr Tyr Ala Ile Thr Ala
 100 105 110

Ala Gly Val Ala His Ala Val Thr Ala Ala Cys Ser Gln Gly Asn Leu
 115 120 125

Ser Asn Cys Gly Cys Asp Arg Glu Lys Gln Gly Tyr Tyr Asn Gln Ala
 130 135 140

Glu Gly Trp Lys Trp Gly Gly Cys Ser Ala Asp Val Arg Tyr Gly Ile
 145 150 155 160

Asp Phe Ser Arg Arg Phe Val Asp Ala Arg Glu Ile Lys Lys Asn Ala
 165 170 175

Arg Arg Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg Lys Val Leu
 180 185 190

Glu Asp Arg Met Gln Leu Glu Cys Lys Cys His Gly Val Ser Gly Ser
 195 200 205

Cys Thr Thr Lys Thr Cys Trp Thr Thr Leu Pro Lys Phe Arg Glu Val
 210 215 220

Gly His Leu Leu Lys Glu Lys Tyr Asn Ala Ala Val Gln Val Glu Val
 225 230 235 240

Val Arg Ala Ser Arg Leu Arg Gln Pro Thr Phe Leu Arg Ile Lys Gln
 245 250 255

Leu Arg Ser Tyr Gln Lys Pro Met Glu Thr Asp Leu Val Tyr Ile Glu
 260 265 270

Lys Ser Pro Asn Tyr Cys Glu Glu Asp Ala Ala Thr Gly Ser Val Gly
 275 280 285

Thr Gln Gly Arg Leu Cys Asn Arg Thr Ser Pro Gly Ala Asp Gly Cys
 290 295 300

Asp Thr Met Cys Cys Gly Arg Gly Tyr Asn Thr His Gln Tyr Thr Lys
 305 310 315 320

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340	345	350
<210> SEQ ID NO 34		
<211> LENGTH: 351		
<212> TYPE: PRT		
<213> ORGANISM: Homo sapiens		
<400> SEQUENCE: 34		
Met Phe Leu Ser Lys Pro Ser Val Tyr Ile Cys Leu Phe Thr Cys Val		
1 5 10 15		
Leu Gln Leu Ser His Ser Trp Ser Val Asn Asn Phe Leu Met Thr Gly		
20 25 30		
Pro Lys Ala Tyr Leu Ile Tyr Ser Ser Ser Val Ala Ala Gly Ala Gln		
35 40 45		
Ser Gly Ile Glu Glu Cys Lys Tyr Gln Phe Ala Trp Asp Arg Trp Asn		
50 55 60		
Cys Pro Glu Arg Ala Leu Gln Leu Ser Ser His Gly Gly Leu Arg Ser		
65 70 75 80		
Ala Asn Arg Glu Thr Ala Phe Val His Ala Ile Ser Ser Ala Gly Val		
85 90 95		
Met Tyr Thr Leu Thr Arg Asn Cys Ser Leu Gly Asp Phe Asp Asn Cys		
100 105 110		
Gly Cys Asp Asp Ser Arg Asn Gly Gln Leu Gly Gly Gln Gly Trp Leu		
115 120 125		
Trp Gly Gly Cys Ser Asp Asn Val Gly Phe Gly Glu Ala Ile Ser Lys		
130 135 140		
Gln Phe Val Asp Ala Leu Glu Thr Gly Gln Asp Ala Arg Ala Ala Met		
145 150 155 160		
Asn Leu His Asn Asn Glu Ala Gly Arg Lys Ala Val Lys Gly Thr Met		
165 170 175		
Lys Arg Thr Cys Lys Cys His Gly Val Ser Gly Ser Cys Thr Thr Gln		
180 185 190		
Thr Cys Trp Leu Gln Leu Pro Glu Phe Arg Glu Val Gly Ala His Leu		
195 200 205		
Lys Glu Lys Tyr His Ala Ala Leu Lys Val Asp Leu Leu Gln Gly Ala		
210 215 220		
Gly Asn Ser Ala Ala Gly Arg Gly Ala Ile Ala Asp Thr Phe Arg Ser		
225 230 235 240		
Ile Ser Thr Arg Glu Leu Val His Leu Glu Asp Ser Pro Asp Tyr Cys		
245 250 255		
Leu Glu Asn Lys Thr Leu Gly Leu Leu Gly Thr Glu Gly Arg Glu Cys		
260 265 270		
Leu Arg Arg Gly Arg Ala Leu Gly Arg Trp Glu Arg Arg Ser Cys Arg		
275 280 285		
Arg Leu Cys Gly Asp Cys Gly Leu Ala Val Glu Glu Arg Arg Ala Glu		
290 295 300		
Thr Val Ser Ser Cys Asn Cys Lys Phe His Trp Cys Cys Ala Val Arg		
305 310 315 320		
Cys Glu Gln Cys Arg Arg Arg Val Thr Lys Tyr Phe Cys Ser Arg Ala		
325 330 335		
Glu Arg Pro Arg Gly Gly Ala Ala His Lys Pro Gly Arg Lys Pro		
340 345 350		

<210> SEQ ID NO 35

<211> LENGTH: 365

-continued

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 35

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Met Leu Asp Gly Ser Pro Leu Ala Arg Trp Leu Ala Ala Ala Phe Gly
1      5      10      15
Leu Thr Leu Leu Leu Ala Ala Leu Arg Pro Ser Ala Ala Tyr Phe Gly
      20      25      30
Leu Thr Gly Ser Glu Pro Leu Thr Ile Leu Pro Leu Thr Leu Glu Pro
      35      40      45
Glu Ala Ala Ala Gln Ala His Tyr Lys Ala Cys Asp Arg Leu Lys Leu
      50      55      60
Glu Arg Lys Gln Arg Arg Met Cys Arg Arg Asp Pro Gly Val Ala Glu
      65      70      75      80
Thr Leu Val Glu Ala Val Ser Met Ser Ala Leu Glu Cys Gln Phe Gln
      85      90      95
Phe Arg Phe Glu Arg Trp Asn Cys Thr Leu Glu Gly Arg Tyr Arg Ala
      100     105     110
Ser Leu Leu Lys Arg Gly Phe Lys Glu Thr Ala Phe Leu Tyr Ala Ile
      115     120     125
Ser Ser Ala Gly Leu Thr His Ala Leu Ala Lys Ala Cys Ser Ala Gly
      130     135     140
Arg Met Glu Arg Cys Thr Cys Asp Glu Ala Pro Asp Leu Glu Asn Arg
      145     150     155     160
Glu Ala Trp Gln Trp Gly Gly Cys Gly Asp Asn Leu Lys Tyr Ser Ser
      165     170     175
Lys Phe Val Lys Glu Phe Leu Gly Arg Arg Ser Ser Lys Asp Leu Arg
      180     185     190
Ala Arg Val Asp Phe His Asn Asn Leu Val Gly Val Lys Val Ile Lys
      195     200     205
Ala Gly Val Glu Thr Thr Cys Lys Cys His Gly Val Ser Gly Ser Cys
      210     215     220
Thr Val Arg Thr Cys Trp Arg Gln Leu Ala Pro Phe His Glu Val Gly
      225     230     235     240
Lys His Leu Lys His Lys Tyr Glu Thr Ala Leu Lys Val Gly Ser Thr
      245     250     255
Thr Asn Glu Ala Ala Gly Glu Ala Gly Ala Ile Ser Pro Pro Arg Gly
      260     265     270
Arg Ala Ser Gly Ala Gly Gly Ser Asp Pro Leu Pro Arg Thr Pro Glu
      275     280     285
Leu Val His Leu Asp Asp Ser Pro Ser Phe Cys Leu Ala Gly Arg Phe
      290     295     300
Ser Pro Gly Thr Ala Gly Arg Arg Cys His Arg Glu Lys Asn Cys Glu
      305     310     315     320
Ser Ile Cys Cys Gly Arg Gly His Asn Thr Gln Ser Arg Val Val Thr
      325     330     335
Arg Pro Cys Gln Cys Gln Val Arg Trp Cys Cys Tyr Val Glu Cys Arg
      340     345     350
Gln Cys Thr Gln Arg Glu Glu Val Tyr Thr Cys Lys Gly
      355     360     365

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<210> SEQ ID NO 36

<211> LENGTH: 357

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 36

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Met Arg Pro Pro Pro Ala Leu Ala Leu Ala Gly Leu Cys Leu Leu Ala
1      5      10      15
Leu Pro Ala Ala Ala Ala Ser Tyr Phe Gly Leu Thr Gly Arg Glu Val
20      25      30
Leu Thr Pro Phe Pro Gly Leu Gly Thr Ala Ala Ala Pro Ala Gln Gly
35      40      45
Gly Ala His Leu Lys Gln Cys Asp Leu Leu Lys Leu Ser Arg Arg Gln
50      55      60
Lys Gln Leu Cys Arg Arg Glu Pro Gly Leu Ala Glu Thr Leu Arg Asp
65      70      75      80
Ala Ala His Leu Gly Leu Leu Glu Cys Gln Phe Gln Phe Arg His Glu
85      90      95
Arg Trp Asn Cys Ser Leu Glu Gly Arg Met Gly Leu Leu Lys Arg Gly
100     105     110
Phe Lys Glu Thr Ala Phe Leu Tyr Ala Val Ser Ser Ala Ala Leu Thr
115     120     125
His Thr Leu Ala Arg Ala Cys Ser Ala Gly Arg Met Glu Arg Cys Thr
130     135     140
Cys Asp Asp Ser Pro Gly Leu Glu Ser Arg Gln Ala Trp Gln Trp Gly
145     150     155     160
Val Cys Gly Asp Asn Leu Lys Tyr Ser Thr Lys Phe Leu Ser Asn Phe
165     170     175
Leu Gly Ser Lys Arg Gly Asn Lys Asp Leu Arg Ala Arg Ala Asp Ala
180     185     190
His Asn Thr His Val Gly Ile Lys Ala Val Lys Ser Gly Leu Arg Thr
195     200     205
Thr Cys Lys Cys His Gly Val Ser Gly Ser Cys Ala Val Arg Thr Cys
210     215     220
Trp Lys Gln Leu Ser Pro Phe Arg Glu Thr Gly Gln Val Leu Lys Leu
225     230     235     240
Arg Tyr Asp Ser Ala Val Lys Val Ser Ser Ala Thr Asn Glu Ala Leu
245     250     255
Gly Arg Leu Glu Leu Trp Ala Pro Ala Arg Gln Gly Ser Leu Thr Lys
260     265     270
Gly Leu Ala Pro Arg Ser Gly Asp Leu Val Tyr Met Glu Asp Ser Pro
275     280     285
Ser Phe Cys Arg Pro Ser Lys Tyr Ser Pro Gly Thr Ala Gly Arg Val
290     295     300
Cys Ser Arg Glu Ala Ser Cys Ser Ser Leu Cys Cys Gly Arg Gly Tyr
305     310     315     320
Asp Thr Gln Ser Arg Leu Val Ala Phe Ser Cys His Cys Gln Val Gln
325     330     335
Trp Cys Cys Tyr Val Glu Cys Gln Gln Cys Val Gln Glu Glu Leu Val
340     345     350
Tyr Thr Cys Lys His
355

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<210> SEQ ID NO 37

<211> LENGTH: 417

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 37

Met 1	Gly	Ser	Ala	His 5	Pro	Arg	Pro	Trp	Leu 10	Arg	Leu	Arg	Pro	Gln	Pro 15
Gln	Pro	Arg	Pro 20	Ala	Leu	Trp	Val	Leu 25	Leu	Phe	Phe	Leu	Leu 30	Leu	Leu
Ala	Ala	Ala	Met 35	Pro	Arg	Ser	Ala 40	Pro	Asn	Asp	Ile	Leu 45	Asp	Leu	Arg
Leu	Pro	Pro	Glu 50	Pro	Val	Leu 55	Asn	Ala	Asn	Thr	Val 60	Cys	Leu	Thr	Leu
Pro 65	Gly	Leu	Ser	Arg	Arg 70	Gln	Met	Glu	Val	Cys 75	Val	Arg	His	Pro	Asp 80
Val	Ala	Ala	Ser 85	Ala	Ile	Gln	Gly	Ile 90	Gln	Ile	Ala	Ile	His	Glu 95	Cys
Gln	His	Gln	Phe 100	Arg	Asp	Gln	Arg	Trp 105	Asn	Cys	Ser	Ser	Leu 110	Glu	Thr
Arg	Asn	Lys	Ile 115	Pro	Tyr	Glu	Ser	Pro 120	Ile	Phe	Ser	Arg 125	Gly	Phe	Arg
Glu	Ser	Ala	Phe 130	Ala	Tyr	Ala 135	Ile	Ala	Ala	Ala	Gly 140	Val	Val	His	Ala
Val 145	Ser	Asn	Ala	Cys	Ala 150	Leu	Gly	Lys	Leu	Lys 155	Ala	Cys	Gly	Cys	Asp 160
Ala	Ser	Arg	Arg 165	Gly	Asp	Glu	Glu	Ala 170	Phe	Arg	Arg	Lys	Leu 175	His	Arg
Leu	Gln	Leu	Asp 180	Ala	Leu	Gln	Arg	Gly 185	Lys	Gly	Leu	Ser	His 190	Gly	Val
Pro	Glu	His	Pro 195	Ala	Leu	Pro	Thr 200	Ala	Ser	Pro	Gly 205	Leu	Gln	Asp	Ser
Trp 210	Glu	Trp	Gly	Gly	Cys	Ser 215	Pro	Asp	Met	Gly 220	Phe	Gly	Glu	Arg	Phe
Ser 225	Lys	Asp	Phe	Leu	Asp 230	Ser	Arg	Glu	Pro	His 235	Arg	Asp	Ile	His	Ala 240
Arg	Met	Arg	Leu 245	His	Asn	Asn	Arg	Val	Gly 250	Arg	Gln	Ala	Val	Met	Glu 255
Asn	Met	Arg	Arg 260	Lys	Cys	Lys	Cys	His 265	Gly	Thr	Ser	Gly 270	Ser	Cys	Gln
Leu	Lys	Thr	Cys 275	Trp	Gln	Val	Thr 280	Pro	Glu	Phe	Arg	Thr 285	Val	Gly	Ala
Leu 290	Leu	Arg	Ser	Arg	Phe 295	His	Arg	Ala	Thr	Leu	Ile 300	Arg	Pro	His	Asn
Arg 305	Asn	Gly	Gly	Gln	Leu 310	Glu	Pro	Gly	Pro	Ala 315	Gly	Ala	Pro	Ser	Pro 320
Ala	Pro	Gly	Ala 325	Pro	Gly	Pro	Arg	Arg	Arg	Ala 330	Ser	Pro	Ala	Asp	Leu 335
Val	Tyr	Phe	Glu 340	Lys	Ser	Pro	Asp	Phe 345	Cys	Glu	Arg	Glu 350	Pro	Arg	Leu
Asp	Ser	Ala	Gly 355	Thr	Val	Gly	Arg	Leu 360	Cys	Asn	Lys	Ser 365	Ser	Ala	Gly
Ser 370	Asp	Gly	Cys	Gly	Ser 375	Met	Cys	Cys	Gly	Arg	Gly 380	His	Asn	Ile	Leu
Arg 385	Gln	Thr	Arg	Ser	Glu 390	Arg	Cys	His	Cys	Arg 395	Phe	His	Trp	Cys	Cys 400
Phe	Val	Val	Cys 405	Glu	Glu	Cys	Arg	Ile 410	Thr	Glu	Trp	Val	Ser	Val	Cys 415

-continued

Lys

<210> SEQ ID NO 38

<211> LENGTH: 389

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 38

Met Leu Glu Glu Pro Arg Pro Arg Pro Pro Pro Ser Gly Leu Ala Gly
 1 5 10 15
 Leu Leu Phe Leu Ala Leu Cys Ser Arg Ala Leu Ser Asn Glu Ile Leu
 20 25 30
 Gly Leu Lys Leu Pro Gly Glu Pro Pro Leu Thr Ala Asn Thr Val Cys
 35 40 45
 Leu Thr Leu Ser Gly Leu Ser Lys Arg Gln Leu Gly Leu Cys Leu Arg
 50 55 60
 Asn Pro Asp Val Thr Ala Ser Ala Leu Gln Gly Leu His Ile Ala Val
 65 70 75 80
 His Glu Cys Gln His Gln Leu Arg Asp Gln Arg Trp Asn Cys Ser Ala
 85 90 95
 Leu Glu Gly Gly Gly Arg Leu Pro His His Ser Ala Ile Leu Lys Arg
 100 105 110
 Gly Phe Arg Glu Ser Ala Phe Ser Phe Ser Met Leu Ala Ala Gly Val
 115 120 125
 Met His Ala Val Ala Thr Ala Cys Ser Leu Gly Lys Leu Val Ser Cys
 130 135 140
 Gly Cys Gly Trp Lys Gly Ser Gly Glu Gln Asp Arg Leu Arg Ala Lys
 145 150 155 160
 Leu Leu Gln Leu Gln Ala Leu Ser Arg Gly Lys Ser Phe Pro His Ser
 165 170 175
 Leu Pro Ser Pro Gly Pro Gly Ser Ser Pro Ser Pro Gly Pro Gln Asp
 180 185 190
 Thr Trp Glu Trp Gly Gly Cys Asn His Asp Met Asp Phe Gly Glu Lys
 195 200 205
 Phe Ser Arg Asp Phe Leu Asp Ser Arg Glu Ala Pro Arg Asp Ile Gln
 210 215 220
 Ala Arg Met Arg Ile His Asn Asn Arg Val Gly Arg Gln Val Val Thr
 225 230 235 240
 Glu Asn Leu Lys Arg Lys Cys Lys Cys His Gly Thr Ser Gly Ser Cys
 245 250 255
 Gln Phe Lys Thr Cys Trp Arg Ala Ala Pro Glu Phe Arg Ala Val Gly
 260 265 270
 Ala Ala Leu Arg Glu Arg Leu Gly Arg Ala Ile Phe Ile Asp Thr His
 275 280 285
 Asn Arg Asn Ser Gly Ala Phe Gln Pro Arg Leu Arg Pro Arg Arg Leu
 290 295 300
 Ser Gly Glu Leu Val Tyr Phe Glu Lys Ser Pro Asp Phe Cys Glu Arg
 305 310 315 320
 Asp Pro Thr Met Gly Ser Pro Gly Thr Arg Gly Arg Ala Cys Asn Lys
 325 330 335
 Thr Ser Arg Leu Leu Asp Gly Cys Gly Ser Leu Cys Cys Gly Arg Gly
 340 345 350
 His Asn Val Leu Arg Gln Thr Arg Val Glu Arg Cys His Cys Arg Phe
 355 360 365

-continued

His Trp Cys Cys Tyr Val Leu Cys Asp Glu Cys Lys Val Thr Glu Trp
 370 375 380

Val Asn Val Cys Lys
 385

<210> SEQ ID NO 39
 <211> LENGTH: 354
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 39

Met Arg Ala Arg Pro Gln Val Cys Glu Ala Leu Leu Phe Ala Leu Ala
 1 5 10 15

Leu Gln Thr Gly Val Cys Tyr Gly Ile Lys Trp Leu Ala Leu Ser Lys
 20 25 30

Thr Pro Ser Ala Leu Ala Leu Asn Gln Thr Gln His Cys Lys Gln Leu
 35 40 45

Glu Gly Leu Val Ser Ala Gln Val Gln Leu Cys Arg Ser Asn Leu Glu
 50 55 60

Leu Met His Thr Val Val His Ala Ala Arg Glu Val Met Lys Ala Cys
 65 70 75 80

Arg Arg Ala Phe Ala Asp Met Arg Trp Asn Cys Ser Ser Ile Glu Leu
 85 90 95

Ala Pro Asn Tyr Leu Leu Asp Leu Glu Arg Gly Thr Arg Glu Ser Ala
 100 105 110

Phe Val Tyr Ala Leu Ser Ala Ala Ala Ile Ser His Ala Ile Ala Arg
 115 120 125

Ala Cys Thr Ser Gly Asp Leu Pro Gly Cys Ser Cys Gly Pro Val Pro
 130 135 140

Gly Glu Pro Pro Gly Pro Gly Asn Arg Trp Gly Gly Cys Ala Asp Asn
 145 150 155 160

Leu Ser Tyr Gly Leu Leu Met Gly Ala Lys Phe Ser Asp Ala Pro Met
 165 170 175

Lys Val Lys Lys Thr Gly Ser Gln Ala Asn Lys Leu Met Arg Leu His
 180 185 190

Asn Ser Glu Val Gly Arg Gln Ala Leu Arg Ala Ser Leu Glu Met Lys
 195 200 205

Cys Lys Cys His Gly Val Ser Gly Ser Cys Ser Ile Arg Thr Cys Trp
 210 215 220

Lys Gly Leu Gln Glu Leu Gln Asp Val Ala Ala Asp Leu Lys Thr Arg
 225 230 235 240

Tyr Leu Ser Ala Thr Lys Val Val His Arg Pro Met Gly Thr Arg Lys
 245 250 255

His Leu Val Pro Lys Asp Leu Asp Ile Arg Pro Val Lys Asp Ser Glu
 260 265 270

Leu Val Tyr Leu Gln Ser Ser Pro Asp Phe Cys Met Lys Asn Glu Lys
 275 280 285

Val Gly Ser His Gly Thr Gln Asp Arg Gln Cys Asn Lys Thr Ser Asn
 290 295 300

Gly Ser Asp Ser Cys Asp Leu Met Cys Cys Gly Arg Gly Tyr Asn Pro
 305 310 315 320

Tyr Thr Asp Arg Val Val Glu Arg Cys His Cys Lys Tyr His Trp Cys
 325 330 335

Cys Tyr Val Thr Cys Arg Arg Cys Glu Arg Thr Val Glu Arg Tyr Val
 340 345 350

-continued

Cys Lys

<210> SEQ ID NO 40

<211> LENGTH: 365

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 40

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Met Asp Arg Ala Ala Leu Leu Gly Leu Ala Arg Leu Cys Ala Leu Trp
1          5          10          15

Ala Ala Leu Leu Val Leu Phe Pro Tyr Gly Ala Gln Gly Asn Trp Met
          20          25          30

Trp Leu Gly Ile Ala Ser Phe Gly Val Pro Glu Lys Leu Gly Cys Ala
          35          40          45

Asn Leu Pro Leu Asn Ser Arg Gln Lys Glu Leu Cys Lys Arg Lys Pro
50          55          60

Tyr Leu Leu Pro Ser Ile Arg Glu Gly Ala Arg Leu Gly Ile Gln Glu
65          70          75          80

Cys Gly Ser Gln Phe Arg His Glu Arg Trp Asn Cys Met Ile Thr Ala
          85          90          95

Ala Ala Thr Thr Ala Pro Met Gly Ala Ser Pro Leu Phe Gly Tyr Glu
          100          105          110

Leu Ser Ser Gly Thr Lys Glu Thr Ala Phe Ile Tyr Ala Val Met Ala
          115          120          125

Ala Gly Leu Val His Ser Val Thr Arg Ser Cys Ser Ala Gly Asn Met
          130          135          140

Thr Glu Cys Ser Cys Asp Thr Thr Leu Gln Asn Gly Gly Ser Ala Ser
145          150          155          160

Glu Gly Trp His Trp Gly Gly Cys Ser Asp Asp Val Gln Tyr Gly Met
          165          170          175

Trp Phe Ser Arg Lys Phe Leu Asp Phe Pro Ile Gly Asn Thr Thr Gly
          180          185          190

Lys Glu Asn Lys Val Leu Leu Ala Met Asn Leu His Asn Asn Glu Ala
          195          200          205

Gly Arg Gln Ala Val Ala Lys Leu Met Ser Val Asp Cys Arg Cys His
          210          215          220

Gly Val Ser Gly Ser Cys Ala Val Lys Thr Cys Trp Lys Thr Met Ser
225          230          235          240

Ser Phe Glu Lys Ile Gly His Leu Leu Lys Asp Lys Tyr Glu Asn Ser
          245          250          255

Ile Gln Ile Ser Asp Lys Thr Lys Arg Lys Met Arg Arg Arg Glu Lys
          260          265          270

Asp Gln Arg Lys Ile Pro Ile His Lys Asp Asp Leu Leu Tyr Val Asn
          275          280          285

Lys Ser Pro Asn Tyr Cys Val Glu Asp Lys Lys Leu Gly Ile Pro Gly
          290          295          300

Thr Gln Gly Arg Glu Cys Asn Arg Thr Ser Glu Gly Ala Asp Gly Cys
305          310          315          320

Asn Leu Leu Cys Cys Gly Arg Gly Tyr Asn Thr His Val Val Arg His
          325          330          335

Val Glu Arg Cys Glu Cys Lys Phe Ile Trp Cys Cys Tyr Val Arg Cys
          340          345          350

Arg Arg Cys Glu Ser Met Thr Asp Val His Thr Cys Lys
          355          360          365

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<210> SEQ ID NO 41
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(31)
<223> OTHER INFORMATION: Forward primer

<400> SEQUENCE: 41

gcatggatcc accatgaacc ggaaagcgcg g

31

<210> SEQ ID NO 42
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(34)
<223> OTHER INFORMATION: Reverse primer

<400> SEQUENCE: 42

gcatgcggcc gctcacttgc acgtgtacat ctcc

34

<210> SEQ ID NO 43
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(33)
<223> OTHER INFORMATION: Forward primer

<400> SEQUENCE: 43

atgggcctgg acgaggccca gtttcagttc cgc

33

<210> SEQ ID NO 44
<211> LENGTH: 33
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(33)
<223> OTHER INFORMATION: Reverse primer

<400> SEQUENCE: 44

gcggaactga aactgggcct cgtccaggcc cat

33

<210> SEQ ID NO 45
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(28)
<223> OTHER INFORMATION: Forward primer

<400> SEQUENCE: 45

gtgccacggc gtggcaggct cgtgcacc

28

<210> SEQ ID NO 46
<211> LENGTH: 28
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(28)

<223> OTHER INFORMATION: Reverse primer

<400> SEQUENCE: 46

gggtgcacgag cctgccacgc cgtggcac

28

The invention claimed is:

1. A modified Wnt7a polypeptide comprising one or more amino acids that reduce lipidation of the Wnt7a polypeptide, wherein said modified Wnt7a polypeptide comprises an amino acid deletion, insertion, or substitution of Cys73 or Ser206.

2. The modified Wnt7a polypeptide of claim 1, wherein the modified Wnt7a polypeptide activates a non-canonical Wnt signaling pathway.

3. A modified Wnt7a polypeptide having decreased lipidation relative to the lipidation of the Wnt7a polypeptide corresponding to any one of SEQ ID NOs: 2 and 6-11, wherein said modified Wnt7a polypeptide comprise an amino acid deletion, insertion, or substitution of Cys73 or Ser206 of any one of SEQ ID NOs: 2 and 6-11.

4. The modified Wnt7a polypeptide of claim 3, wherein the polypeptide comprises:

- a) an amino acid deletion, insertion, or substitution at the amino acid position corresponding to position 73 of any one of SEQ ID NOs: 2 and 6-11;
- b) an amino acid deletion, insertion, or substitution at the amino acid position corresponding to position 206 of any one of SEQ ID NOs: 2 and 6-11;
- c) one or more amino acid deletions, insertions, or substitutions at the amino acid positions corresponding to positions 73 and 206 of any one of SEQ ID NOs: 2 and 6-11;
- d) an Alanine at the amino acid position corresponding to position 73 or 206 of any one of SEQ ID NOs: 2 and 6-11; or
- e) an Alanine at the amino acid positions corresponding to positions 73 and 206 of any of SEQ ID NOs: 2 and 6-11.

5. A polynucleotide encoding the modified Wnt7a polypeptide of claim 1.

6. A vector comprising the polynucleotide of claim 5.

7. A host cell comprising the vector of claim 6.

8. A modified Wnt7a polypeptide produced by the host cell of claim 7.

9. A composition comprising the polypeptide of claim 8.

10. A method for treating or preventing muscle loss comprising administering to a subject a composition according to claim 9.

11. The method of claim 10, wherein the subject has or is at risk of having a disease or condition affecting muscle.

12. The method of claim 11, wherein the degenerative disease is muscular dystrophy.

13. The method of claim 11, wherein the disease or condition affecting muscle is a wasting disease, muscular attenuation, muscle atrophy, ICU-induced weakness, prolonged disuse, surgery-induced weakness, or a muscle degenerative disease.

14. A Wnt7a polypeptide comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 3-5, and 12-13.

15. A fusion polypeptide comprising a Wnt7a polypeptide according to claim 14 and a native signal peptide, a heterologous signal peptide, a hybrid of a native and a heterologous signal peptide, a heterologous protease cleavage site, an epitope tag or an immunoglobulin Fc region.

16. The fusion polypeptide of claim 15, wherein the heterologous signal peptide is selected from the group consisting of:

- a) a CD33 signal peptide, an immunoglobulin signal peptide, a growth hormone signal peptide, an erythropoietin signal peptide, an albumin signal peptide, a secreted alkaline phosphatase signal peptide, and a viral signal peptide; or
- b) a CD33 signal peptide, an IgGκ signal peptide, and a IgGμ signal peptide.

17. The fusion polypeptide of claim 15, comprising a heterologous protease cleavage site or an epitope tag.

18. The fusion polypeptide of claim 15, wherein the fusion polypeptide comprising an amino acid sequence as set forth in any one of SEQ ID NOs: 3-5 and 12-13, has increased production, secretion, or solubility compared to a corresponding native Wnt polypeptide as set forth in SEQ ID NOs: 2 and 6-11.

* * * * *